

PS Disclosure; Fig 1B; 189pp; English.

The invention relates to a novel isolated polynucleotide comprising a dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-like molecule (DCLH) gene. The polynucleotide of the invention demonstrates anti-allergic and immunosuppressive activities and may be useful for treating a condition including an allergy such as asthma, allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as diabetes mellitus or rheumatoid arthritis or transplant rejection. Furthermore, the polynucleotide may be useful as a vaccine or during gene therapy procedures. The genetically modified animal or the identified modulatory agent of the invention may be used in the study of immunity, DC function, brain physiology or neuronal cell function. The current sequence is that of the human DCLH protein (SEQ ID 4) of the invention which is encoded by the human DCLH cDNA.

SQ Sequence 530 AA;

Query March	100.0%	Score 2781	DB 7	Length 530
Best Local Similarity	100.0%	Pred. NC 9.2e-268		
Matches 530	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	1	MSNPDMPLPGGEELKOKAEJEDAEKXSPATVYKAKKOIOADDMOEETKPTTGR	60
Db	1	MSNPDMPLPGGEELKOKAEJEDAEKXSPATVYKAKKOIOADDMOEETKPTTGR	60
Qy	61	RSLSRSISOSSTDYSSAASYTSDSDDEVSPREKOOTNSKSSNFCVYNIKQAEFGRREI	120
Db	61	RSLSRSISOSSTDYSSAASYTSDSDDEVSPREKOOTNSKSSNFCVYNIKQAEFGRREI	120
Qy	121	ETAEODMSALTSRKRROGEKPLAGAKTVGCHTIAOTAVLIEITLCALGAQCRMSACNIX	180
Db	121	ETAEODMSALTSRKRROGEKPLAGAKTVGCHTIAOTAVLIEITLCALGAQCRMSACNIX	180
Qy	181	STONEVAALAAEAGVAFAMKGESEDDFWMCIDRCVNNDMQAMNILLDDGGDLTHWYKK	240
Db	181	STONEVAALAAEAGVAFAMKGESEDDFWMCIDRCVNNDMQAMNILLDDGGDLTHWYKK	240
Qy	241	YHPVEKIRIGIYEESVTGVRHLYOLSKYKXCVPMANVNDSTVKOKPDNYCCRESEILDG	300
Db	241	YHPVEKIRIGIYEESVTGVRHLYOLSKYKXCVPMANVNDSTVKOKPDNYCCRESEILDG	300
Qy	301	LKRITDVMFGKQVYVCGYGEVKGCCALKALGAIYVITEIDETICALQACMDGFRVVKL	360
Db	301	LKRITDVMFGKQVYVCGYGEVKGCCALKALGAIYVITEIDETICALQACMDGFRVVKL	360
Qy	361	NEYIROVDVITCTGNKXVYTRERHLDPMKNSCTVCNMHSTETEDYTSLRPELTWRRVR	420
Db	361	NEYIROVDVITCTGNKXVYTRERHLDPMKNSCTVCNMHSTETEDYTSLRPELTWRRVR	420
Qy	421	SOVDHYIWPDGKRVLLAEGRLNLSCTVPFVLSIATTTQALALIELYNAPEGGRKOD	480
Db	421	SOVDHYIWPDGKRVLLAEGRLNLSCTVPFVLSIATTTQALALIELYNAPEGGRKOD	480
Qy	481	VYLLPDKMDEYASLHLSBFDALHTEITDDQAKYIGLNKGPFKPNYYR	530
Db	481	VYLLPDKMDEYASLHLSBFDALHTEITDDQAKYIGLNKGPFKPNYYR	530

RESULT 2
ADB68450
ID ADB68450 standard; protein; 530 AA

AC ADB684507

DT 04-DEC-2003 (first entry)

DE Murine DCAL protein - .SEQ ID 6.

KM dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
KM DC, AHCV, DCAL, antiallergic; immunosuppressive; allergy; asthma;
KM allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
KM rheumatoid arthritis; transplant rejection; vaccine; gene therapy;

KW murine; mouse

OS Mus. sp.

FH Key

ET

PN WO20030

PD 10-JUL-

PF 24-DEC-

PR 24-DEC-

PA (ORDE-)

PI Kato M,

DR WPI; 20

XX
DE 11-1-73

PT	molecule
PT	...

PT reject

PS Disclos

CC The inv

CC Like me

CC useful

CC Firstborn

The invention relates to a novel isolated polynucleotide comprising a dendritic cell (DC)-expressed 5'-adenosyl homocysteine hydrolase (AHCY)-like molecule (DCLAL) gene. The polynucleotide of the invention demonstrates antiallergic and immunosuppressive activities and may be used for treating a condition including an allergy such as asthma, allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as diabetes mellitus or rheumatoid arthritis or transplant rejection. Furthermore, the polynucleotide may be useful as a vaccine or during gene therapy procedures. The genetically modified animal or the identified molecular agent of the invention may be used in the study of immunity, DC function, brain physiology or neuronal cell function. The current sequence is that of the murine DCLAL protein (SEQ ID 6) of the invention which is encoded by genomic DNA.

SQ Sequence 530 AA;

Query Match	100.0%	Score 2781	DB 7	Length 530
Similarity	100.0%	Pred. No. 9	2e-268	
Best Local				
Matches 530	0	Mismatches 0	Indels 0	Gaps 0
Conservative				

Qy	1	MEMPAMPLPGVEGELKQAKIIEDIAEKXSPAAVTTKPKQIQFADMOGFTKPKTKGR	60
Db	1	MEMPAMPLPGVEGELKQAKIIEDIAEKXSPAAVTTKPKQIQFADMOGFTKPKTKGR	60
Qy	61	RLSLRSISOSTSDTSSAASYTDSDDVEPREKQOQNSKSGSNFCYKNIKQAFGRREI	120
Db	61	RLSLRSISOSTSDTSSAASYTDSDDVEPREKQOQNSKSGSNFCYKNIKQAFGRREI	120
Qy	121	ELAEDOMGSLISLRRAQGEKPLAGAKIVGCTHTTAOTAVLIETLCALGAQCRMSACNII	180
Db	121	ELAEDOMGSLISLRRAQGEKPLAGAKIVGCTHTTAOTAVLIETLCALGAQCRMSACNII	180
Qy	181	STONVVAALALAGAYAVPAFKGESEDDFWNCIDPCVNMDGMOANMLIDDSGDLTHWVYKK	240
Db	181	STONVVAALALAGAYAVPAFKGESEDDFWNCIDPCVNMDGMOANMLIDDSGDLTHWVYKK	240
Qy	241	YENFVKIRIGIYESVTGVRHLYOLSLPAGKLCVPAVMNVDSVTXKQFDNLCCRESIIIDG	300
Db	241	YENFVKIRIGIYESVTGVRHLYOLSLPAGKLCVPAVMNVDSVTXKQFDNLCCRESIIIDG	300
Qy	301	LKRTTDMVFGKQVAVCYGVEVGKCCALKALGAIYITIEDIPICLOKCMQMGFRVYKL	360
Db	301	LKRTTDMVFGKQVAVCYGVEVGKCCALKALGAIYITIEDIPICLOKCMQMGFRVYKL	360

PI Mikoshiba K, Ando H, Mizutani A, Matsui-Ura T;
 XX
 DR WPI: 2004-349314/33.
 DR N-PSDB: ADM94433.
 XX
 XX New inositol 1,4,5-trisphosphate receptor-binding protein that binds to
 PT inositol 1,4,5-trisphosphate receptor, useful as inositol 1,4,5-
 PT trisphosphate indicator intracellularly and in cell-free system.
 XX
 XX Claim 1; SEQ ID NO 1; 61pp; English.
 XS

CC The invention relates to a novel inositol 1,4,5-trisphosphate (IP3)
CC receptor-binding protein (1) that binds to IP3 receptor. (1) is used as
CC an IP3 indicator in combination with a fluorescent molecule for detecting
CC IP3 by the fluorescence resonance energy transfer (FRET) method using a
CC combination of two fluorescent molecules applicable to the FRET method,
CC and a protein containing at least IP3-binding domain of IP3 receptor
CC labelled with the other fluorescent molecule. (1) is useful as IP3
CC indicator intracellularly and in cell-free system, for detecting and/or
CC quantifying IP3, as modulator of IP3-induced Ca2+ releasing activity,
CC modulator of IP3 function and Na2+ and bicarbonate ions. This sequence
CC represents the IP3 receptor binding protein.

SQ Sequence 530 AA;

Query Match	100.0%;	Score 2781;	DB 8;	Length 530;
Best Similarity	100.0%;	Pred. No. 9.2e-268;		
Matches 530; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0.

Qy	1	MSMPAMPLPGVGEELKQKKEI	EDBKYSFPM	IVTAPKPKIOFADMOEFKPKTKR	60							
Dp	1	MSMPAMPLPGVGEELKQKKEI	EDBKYSFPM	IVTAPKPKIOFADMOEFKPKTKR	60							
Qy	61	RSLSRSISQSTSDYS	SSAS	TYTDS	SDDEVS	PREKQOTNSKSSNFCVKNI	KQAFGRREI	120				
Dp	61	RSLSRSISQSTSDYS	SSAS	TYTDS	SDDEVS	PREKQOTNSKSSNFCVKNI	KQAFGRREI	120				
Qy	121	ETAEEDMNLISLRKQAGEKPLAGKI	YVGC	THITQ	AVILETTL	CALAQCSWASCN	180					
Dp	121	ETAEEDMNLISLRKQAGEKPLAGKI	YVGC	THITQ	AVILETTL	CALAQCSWASCN	180					
Qy	181	STONEVAALAEAGAVAFAMKES	EDBFM	WCIDRCVNM	GMQAMN	ILDDG	DLTHVYKX	240				
Dp	181	STONEVAALAEAGAVAFAMKES	EDBFM	WCIDRCVNM	GMQAMN	ILDDG	DLTHVYKX	240				
Qy	241	YPNPFKKIRGIYESV	TYG	VHRLYOLSKAGK	CVPMAN	VNDSTVK	KQFDM	LYCCRES	ILDG	300		
Dp	241	YPNPFKKIRGIYESV	TYG	VHRLYOLSKAGK	CVPMAN	VNDSTVK	KQFDM	LYCCRES	ILDG	300		
Qy	301	LKRTTDVWFGGQVYV	CGYGEV	SGCCAL	KALGAV	IT	IEDIP	CALQACMDG	FRVYKL	360		
Dp	301	LKRTTDVWFGGQVYV	CGYGEV	SGCCAL	KALGAV	IT	IEDIP	CALQACMDG	FRVYKL	360		
Qy	361	NEVIRQVDV	VITTC	GNKVY	TREH	LDKMN	SCIVCM	SGHSN	TEIDV	SLTPBEL	THERYA	420
Dp	361	NEVIRQVDV	VITTC	GNKVY	TREH	LDKMN	SCIVCM	SGHSN	TEIDV	SLTPBEL	THERYA	420
Qy	421	SOVBHVPWPGDKRV	LLAEGRL	NLNSC	SVPT	FVLSIT	AT	TQALAI	ELYN	AEGRYKOD	480	
Dp	421	SOVBHVPWPGDKRV	LLAEGRL	NLNSC	SVPT	FVLSIT	AT	TQALAI	ELYN	AEGRYKOD	480	
Qy	481	VYLLPKKDEY	YASLH	PSF	DH	TEL	TDQAK	YGLN	KNGP	KPNYRY	530	
Dp	481	VYLLPKKDEY	YASLH	PSF	DH	TEL	TDQAK	YGLN	KNGP	KPNYRY	530	

RESULT 5
ABM80118
ID ABM80118 standard; protein; 530 AA

XX	Tumour-associated antigenic target (TAT) polypeptide P080619, SEQ.301
DE	
XX	
KW	Tumour-associated antigenic target; TAT; human; overexpression; cancer
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW	central nervous system cancer; bladder cancer; pancreatic cancer;
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;
KW	chromosome identification; chromosome mapping; gene mapping;
KW	gene therapy; cytostatic.

OS Homo sapiens.

PN W02004030615-A2.

PD 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.

PR 02-OCT-2002; 2002US-0414971P.

PA (GETH) GENENTECH INC.

PI Wu TD, Zhang Z, Zhou Y;

DR WPI; 2004-347921/32.

XX
E

PT New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.

Claim 12; SEQ ID NO 301; 7273pp; English.

The invention relates to human tumour-associated antigenic target (TAT) polypeptides, and their related nucleic acids. The TAT polypeptides are overexpressed in cancer tissues compared to normal tissues, and may thus serve as effective targets for the diagnosis and treatment of cancer in mammals. The invention also relates to nucleic acid and polypeptide sequences at least 80% identical to the TAT nucleic acids and polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention.

Sequence 530 AA;

Query Match	100.0%	Score 2781	DB 8	Length 530
Best Local Similarity	100.0%	Pred. No. 9	2e-268	
Matches 530; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

QY	1	MSNPDMAPPLPGVGEELKQAKIEIDAEKYSFPAATVTKAPKQIOFADDMOEFTYKPYITGR	60
		1	MSNPDMAPPLPGVGEELKQAKIEIDAEKYSFPAATVTKAPKQIOFADDMOEFTYKPYITGR
Db			60
QY	61	RSLSRSKTSQSSSTDSTSYSSAASYTDSDDSVSPREKQOQNSKSSNFCVYNKKQAEFGREI	120
		61	RSLSRSKTSQSSSTDSTSYSSAASYTDSDDSVSPREKQOQNSKSSNFCVYNKKQAEFGREI
Db			120
QY	121	ETAEQMSMLILRRRQGEKPLAAKIVGCTHTTAQAVLIELTCLAGACQCSASACNII	180
		121	ETAEQMSMLILRRRQGEKPLAAKIVGCTHTTAQAVLIELTCLAGACQCSASACNII
QY			180

QY 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMNDGQANMILDDGGDLTHWYKK 240
 DB 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMNDGQANMILDDGGDLTHWYKK 240
 QY 241 YPNVFKIRIGVIESVTVGHRLYQLSKAGKLCVPMANVNDSTYKQKFDNLCCRESILDG 300
 DB 241 YPNVFKIRIGVIESVTVGHRLYQLSKAGKLCVPMANVNDSTYKQKFDNLCCRESILDG 300
 QY 301 LKRTTDVWFGKQVAVGGEVGGCCALKALGAIIVYTEIDPICALQACMDGFRVYKL 360
 DB 301 LKRTTDVWFGKQVAVGGEVGGCCALKALGAIIVYTEIDPICALQACMDGFRVYKL 360
 QY 361 NEVIRQVDVITTCGNKVVTRHLDKMNKSCIYCNMGHSTNTEIDVTSLRTPELTWERYR 420
 DB 361 NEVIRQVDVITTCGNKVVTRHLDKMNKSCIYCNMGHSTNTEIDVTSLRTPELTWERYR 420
 QY 421 SOVDHVIMPDGKRVVLAEGRLNLSCSTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
 DB 421 SOVDHVIMPDGKRVVLAEGRLNLSCSTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
 QY 481 VYLLPKKMDDEVVASHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530
 DB 481 VYLLPKKMDDEVVASHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530

RESULT 6
 ADP23045
 ID ADP23045 standard; protein; 530 AA.
 AC ADP23045;
 DT 18-NOV-2004 (first entry)
 DE PRO polypeptide SEQ ID NO:139.
 KM PRO: antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;
 KN osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
 KM antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
 OS Unidentified.
 XX MO2004041170-A2.
 PD 21-MAY-2004.
 PF 30-OCT-2003; 2003WO-US034312.
 PR 01-NOV-2002; 2002US-0423394P.
 PA (GETH) GENENTECH INC.
 PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
 MU TD;
 XX WPI; 2004-419628/39.
 DR N-PSDB; ADP23044.
 PT New PRO polypeptides and polynucleotides, useful for treating e.g.
 PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
 PT renal disease, or demyelinating diseases of the central or peripheral
 PT nervous system.
 PS Claim 7; SEQ ID NO 139; 2940bp; English.
 CC The invention relates to a novel isolated nucleic acid and the PRO
 CC polypeptide encoded by it. A protein of the invention has
 CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,
 CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
 CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
 CC of the invention may have a use in gene therapy. The PRO polypeptide, its
 CC agonist, antagonist, or antibody that specifically binds to the
 CC polypeptide is useful for treating an immune related disorder such as

CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
 CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
 CC idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune
 CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
 CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
 CC disease, a demyelinating disease of the central or peripheral nervous
 CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
 CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
 CC disease, infectious or autoimmune chronic active hepatitis, primary
 CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
 CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
 CC disease, an autoimmune or immune-mediated skin disease, a bulous skin
 CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
 CC disease, asthma, allergic rhinitis, atopic dermatitis, food
 CC hypersensitivity, urticaria, an immunologic disease of the lung,
 CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
 CC pneumonitis, a transplantation associated disease, graft rejection or
 CC graft-versus-host disease. The present sequence represents a PRO protein
 CC of the invention.
 XX

Sequence 530 AA;
 SQ
 Query Match 100.0%; Score 2781; DB 8; Length 530;
 Best Local Similarity 100.0%; Pred. No. 9.2e-268;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPVGEELKQAKIEDEAKYSFMAVTTAKPKKQIQFADDMQEFPTKTKGR 60
 DB 1 MSMPDAMPVGEELKQAKIEDEAKYSFMAVTTAKPKKQIQFADDMQEFPTKTKGR 60
 QY 61 RSLRSISQSSSTDYSSAASATDSSDDESPREKQNTSKGSSNFCVNNIKQAEGRREI 120
 DB 61 RSLRSISQSSSTDYSSAASATDSSDDESPREKQNTSKGSSNFCVNNIKQAEGRREI 120
 QY 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIELTALCAQCRWSACNLY 180
 DB 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIELTALCAQCRWSACNLY 180
 QY 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMNDGQANMILDDGGDLTHWYKK 240
 DB 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMNDGQANMILDDGGDLTHWYKK 240
 QY 241 YPNVFKIRIGVIESVTVGHRLYQLSKAGKLCVPMANVNDSTYKQKFDNLCCRESILDG 300
 DB 241 YPNVFKIRIGVIESVTVGHRLYQLSKAGKLCVPMANVNDSTYKQKFDNLCCRESILDG 300
 QY 301 LKRTTDVWFGKQVAVGGEVGGCCALKALGAIIVYTEIDPICALQACMDGFRVYKL 360
 DB 301 LKRTTDVWFGKQVAVGGEVGGCCALKALGAIIVYTEIDPICALQACMDGFRVYKL 360
 QY 361 NEVIRQVDVITTCGNKVVTRHLDKMNKSCIYCNMGHSTNTEIDVTSLRTPELTWERYR 420
 DB 361 NEVIRQVDVITTCGNKVVTRHLDKMNKSCIYCNMGHSTNTEIDVTSLRTPELTWERYR 420
 QY 421 SOVDHVIMPDGKRVVLAEGRLNLSCSTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
 DB 421 SOVDHVIMPDGKRVVLAEGRLNLSCSTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
 QY 481 VYLLPKKMDDEVVASHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530
 DB 481 VYLLPKKMDDEVVASHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530

RESULT 7
 AAM56097
 ID AAM56097 standard; protein; 614 AA.
 XX
 AC AAM56097;
 XX
 DT 21-AUG-1998 (first entry)
 XX
 DE Amino acid sequence of the ODD4b5.3 enzyme.
 XX

KM DD4b9.3 enzyme; S-adenosyl-L-homocysteine hydrolase-type activity;
 KM AHcy-type activity; stimulation; inhibition; dendritic cell; cancer;
 KM autoimmune disease; transplantation.
 OS Homo sapiens.
 XX MO9814562-A1.
 XX PD 09-APR-1998.
 XX PF 06-OCT-1997; 97MO-NZ000133.
 XX PR 04-OCT-1996; 96NZ-00299507.
 XX (HART/) HART D N J.
 XX Hart DNT;
 XX WPI; 1998-240074/21.
 DR N-PSDB; AAV28617.
 XX
 PT New isolated S-adenosyl-L-homocysteine hydrolase enzyme - is used to
 PT develop products which can be used in the treatment of e.g. auto-immune
 PT disease, transplantations or cancers.
 PS Claim 3; Fig 1, 33pp; English.
 XX
 CC This is the amino acid sequence of the DD4b9.3 enzyme which has S-
 CC adenosyl-L-homocysteine hydrolase (AHcy)-type activity. Its products can
 CC be used to identify substances which have a stimulatory or inhibitory
 CC effect on the enzyme activity. Such substances can be used to modulate
 CC dendritic cell (DC) function and for immunomodulation. They can be used
 CC in the treatment of e.g. autoimmune diseases, transplantations or
 CC cancers. The products can also be used for detection and diagnosis
 CC
 SQ Sequence 614 AA;
 Query Match 100.0%; Score 2781; DB 2; Length 614;
 Best Local Similarity 100.0%; Pred. No. 1.2e-267;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMPDAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMOEFTEFPKTKGR 60
 DB 85 MSMPDAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMOEFTEFPKTKGR 144
 QY 61 RSLRSRISQSSSTDSYSSAASYTDSDEVPSPREKQOTNSKGSNFCVKNIKQAEFGRRRI 120
 DB 145 RSLRSRISQSSSTDSYSSAASYTDSDEVPSPREKQOTNSKGSNFCVKNIKQAEFGRRRI 204
 QY 121 EIAQDMSALISLRKAQGEKPLAGAKIVGCTHTTAQTAVALIETLCAAGQCRWSACNIT 180
 DB 205 EIAQDMSALISLRKAQGEKPLAGAKIVGCTHTTAQTAVALIETLCAAGQCRWSACNIT 264
 QY 181 STONEVRAALAEVGVAFPMKGESEDDFWMCIDRCVMMDSQNMILLDDGGDLTHWYKK 240
 DB 265 STONEVRAALAEVGVAFPMKGESEDDFWMCIDRCVMMDSQNMILLDDGGDLTHWYKK 324
 QY 241 YPVVFKKIRGIVEESTYGVHRLYQLSKAGKLCVPANVNDVSTKQKFDNLYCCRRESILD 300
 DB 325 YPVVFKKIRGIVEESTYGVHRLYQLSKAGKLCVPANVNDVSTKQKFDNLYCCRRESILD 384
 QY 301 LKRTTDMFGGKOVVVGVEVGKCCALKALGAIVYITIEDIPICALQCMGFRVVKL 360
 DB 385 LKRTTDMFGGKOVVVGVEVGKCCALKALGAIVYITIEDIPICALQCMGFRVVKL 444
 QY 361 NEVIRQDVVITCTGKNKVVTRREHLDMKNSCIQNMGSHNTEIDVTSLTPELTWERVR 420
 DB 445 NEVIRQDVVITCTGKNKVVTRREHLDMKNSCIQNMGSHNTEIDVTSLTPELTWERVR 504
 QY 421 SQVDHVIWPDGKRVLLAEGRLLNLSCTVPTFVLSTATTATQALALIELYNAEGRRYKOD 480
 DB 505 SQVDHVIWPDGKRVLLAEGRLLNLSCTVPTFVLSTATTATQALALIELYNAEGRRYKOD 564

QY 481 VLLPKRMDYVASLHLPSEFDAHLELTDQAKYIQLNKGPFKPNYYR 530
 DB 565 VLLPKRMDYVASLHLPSEFDAHLELTDQAKYIQLNKGPFKPNYYR 614
 RESULT 8
 ADB68452
 ID ADB68452 standard; protein; 530 AA.
 XX
 AC ADB68452;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Murine DCAL protein - SEQ ID 8.
 XX
 KM dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
 KM DC; AHcy; DCAL; antiallergic; immunosuppressive; allergy; asthma;
 KM allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
 KM rheumatoid arthritis; transplant rejection; vaccine; gene therapy;
 KM murine; mouse.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 318..323
 FT /note="NAD+ binding motif (GXGXXG)"
 XX
 PN MO2003055997-A1.
 XX
 PD 10-JUL-2003.
 XX
 PF 24-DEC-2002; 2002MO-AU001761.
 XX
 PR 24-DEC-2001; 2001AU-00009741.
 XX
 PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
 XX
 PI Kato M, Angel NZ, Cooper BJ, Hart DNT;
 XX
 DR WPI; 2003-559275/52.
 XX
 DR N-PSDB; ADB68451.
 XX
 PT New dendritic cell expressed S-adenosyl homocysteine hydrolase-like
 PT molecule (DCAL) gene, useful for preparing a composition for treating or
 PT preventing a condition e.g., allergy, autoimmune disease or transplant
 PT rejection.
 XX
 PS Disclosure; Page 175-177; 189pp; English.
 XX
 CC The invention relates to a novel isolated polynucleotide comprising a
 CC dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHcy)-
 CC like molecule (DCAL) gene. The polynucleotide of the invention
 CC demonstrates antiallergic and immunosuppressive activities and may be
 CC useful for treating a condition including an allergy such as asthma,
 CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
 CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
 CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
 CC therapy procedures. The genetically modified animal or the identified
 CC modulatory agent of the invention may be used in the study of immunity,
 CC DC function, brain physiology or neuronal cell function. The current
 CC sequence is that of the murine DCAL protein (SEQ ID 8) of the invention
 CC which is encoded by cDNA.
 XX
 SQ Sequence 530 AA;
 Query Match 99.9%; Score 2778; DB 7; Length 530;
 Best Local Similarity 99.8%; Pred. No. 1.8e-267;
 Matches 529; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMPDAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMOEFTEFPKTKGR 60
 DB 1 MSMPDAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMOEFTEFPKTKGR 60

QY 61 RLSTRSISQSTSDSYSSAASYTSSDDEVSPEKQOOTSNGSSNFCVKNIKOAEFRREI 120
 DB 61 RLSTRSISQSTSDSYSSAASYTSSDDEVSPEKQOOTSNGSSNFCVKNIKOAEFRREI 120
 QY 121 ELAEDQMSALISLRKRAQGEKPLAGAKIVGCTHITQTOTAIVLETLCAQAQCRWSACNII 180
 DB 121 ELAEDQMSALISLRKRAQGEKPLAGAKIVGCTHITQTOTAIVLETLCAQAQCRWSACNII 180
 QY 181 STONEVAALAAAGAVAFVPMKGESEDDFWWCIDRCVNMGMQANMLDGGDLTHWVYK 240
 DB 181 STONEVAALAAAGAVAFVPMKGESEDDFWWCIDRCVNMGMQANMLDGGDLTHWVYK 240
 QY 241 YPNVEFKKIRGIYESVTVGHRLYQLSKAGKLCVPMANVNDSTYKQKFDNLCCRESILDG 300
 DB 241 YPNVEFKKIRGIYESVTVGHRLYQLSKAGKLCVPMANVNDSTYKQKFDNLCCRESILDG 300
 QY 301 LKRTIDVMEFGKQVYVCGYGEVKGCCALKALGAIIVTTEIDPICALQACMDGFRVVL 360
 DB 301 LKRTIDVMEFGKQVYVCGYGEVKGCCALKALGAIIVTTEIDPICALQACMDGFRVVL 360
 QY 361 NEVIRQVDVITCTGNKNVVTREHLDPMKNSCIVCMGHSNTEIDVTSLRTELTWERVR 420
 DB 361 NEVIRQVDVITCTGNKNVVTREHLDPMKNSCIVCMGHSNTEIDVTSLRTELTWERVR 420
 QY 421 SOVDHVIWPDGKRVVLLAEGRLNLSCTVPTFPVLTATTOALALIELYNAPBGRYKOD 480
 DB 421 SOVDHVIWPDGKRVVLLAEGRLNLSCTVPTFPVLTATTOALALIELYNAPBGRYKOD 480
 QY 481 VYLLPKKQDEYVVAASHLPSFDAHTELTDQAKYLGILNKGPFKNYRY 530
 DB 481 VYLLPKKQDEYVVAASHLPSFDAHTELTDQAKYLGILNKGPFKNYRY 530

RESULT 9
 AAM90061
 ID AAM90061 standard; protein; 500 AA.

AC AAM90061;
 DT 04-MAR-1999 (first entry)
 DE Human SAHH protein.
 KM S-adenosyl-5-homocysteine hydrolase; SAHH; human; drug screening;
 KM treatment; infection; cancer; autoimmune disease; detection; diagnosis;
 KM gene mapping; antisense; therapy; antagonist; immunoassay.
 OS Homo sapiens.
 XX US5854023-A.
 PD 29-DEC-1998.
 PF 17-JUL-1997; 97US-00896005.
 PR 17-JUL-1997; 97US-00896005.
 PA (INCY-) INCYTE PHARM INC.
 PI Shah P, Lal P, Hillman JL, Corley NC;
 DR WPI; 1999-094306/08.
 DR N-PSDB; AAV73924.
 PT Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase - for
 PT production of recombinant enzyme, useful for diagnosis, treatment and
 PT prevention of cancers, infections and autoimmune diseases.
 PS Claim 1; Fig 1A-I; 40pp; English.

CC This sequence represents a human S-adenosyl-5-homocysteine hydrolase
 CC (SAHH). The SAHH protein can be used to generate specific antibodies and
 CC in drug screening to identify specific binding agents. Antagonists of the

CC protein are used to treat or prevent a wide range of viral, bacterial,
 CC fungal, parasitic, protozoal or helminthic infections, many cancers
 CC (leukaemia, lymphoma or solid tumours), and many autoimmune diseases
 CC (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes
 CC mellitus, multiple sclerosis etc). All these conditions may be treated by
 CC expressing antisense sequences, triplex-forming agents or ribozymes
 CC directed against the nucleic acid. The nucleic acid and its fragments can
 CC be used as probes or primers for detecting and quantifying gene
 CC expression, for diagnosis or monitoring of disease, to identify genetic
 CC variations, mutations or polymorphisms, in gene mapping and as antisense
 CC therapeutics. Antibodies are used directly as antagonists, indirectly
 CC to deliver active agents to SAHH-expressing cells, to diagnose and monitor
 CC diseases in standard immunoassays, in competitive drug screens and to
 CC isolate the protein from natural sources

Sequence 500 AA;
 Query Match 94.1%; Score 2618; DB 2; Length 500;
 Best Local Similarity 99.8%; Pred. No. 1.5e-251;
 Matches 499; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 31 MATVTKAPKKOIQFADDMQEFTEPTKTGRSLRSISQSTSDSYSSAASYTSSDDEVS 90
 DB 1 MATVTKAPKKOIQFADDMQEFTEPTKTGRSLRSISQSTSDSYSSAASYTSSDDEVS 60
 QY 91 PREKQOOTSNGSSNFCVKNIKOAEFRREIELAEDQMSALISLRKRAQGEKPLAGAKIVG 150
 DB 61 PREKQOOTSNGSSNFCVKNIKOAEFRREIELAEDQMSALISLRKRAQGEKPLAGAKIVG 120
 QY 151 CTHITQTOTAIVLETLCAQAQCRWSACNIIYSTONEVAALAAAGAVAFVPMKGESEDDFW 210
 DB 121 CTHITQTOTAIVLETLCAQAQCRWSACNIIYSTONEVAALAAAGAVAFVPMKGESEDDFW 180
 QY 211 CIDRCVNMGMQANMLDGGDLTHWVYKYPNVEFKKIRGIYESVTVGHRLYQLSKAGK 270
 DB 181 CIDRCVNMGMQANMLDGGDLTHWVYKYPNVEFKKIRGIYESVTVGHRLYQLSKAGK 240
 QY 271 LCVPMANVNDSTYKQKFDNLCCRESILDGILKRTIDVMEFGKQVYVCGYGEVKGCCAL 330
 DB 241 LCVPMANVNDSTYKQKFDNLCCRESILDGILKRTIDVMEFGKQVYVCGYGEVKGCCAL 300
 QY 331 KALGAIIVTTEIDPICALQACMDGFRVVLNEVIRQVDVITCTGNKNVVTREHLDPMKN 390
 DB 301 KALGAIIVTTEIDPICALQACMDGFRVVLNEVIRQVDVITCTGNKNVVTREHLDPMKN 360
 QY 391 SCIVCMGHSNTEIDVTSLRTELTWERVRSQVDHVIWPDGKRVVLLAEGRLNLSCTV 450
 DB 361 SCIVCMGHSNTEIDVTSLRTELTWERVRSQVDHVIWPDGKRVVLLAEGRLNLSCTV 420
 QY 451 PTFVLSTATTOALALIELYNAPBGRYKODVYLLPKKQDEYVVAASHLPSFDAHTELTD 510
 DB 421 PTFVLSTATTOALALIELYNAPBGRYKODVYLLPKKQDEYVVAASHLPSFDAHTELTD 480
 QY 511 QAKYLGILNKGPFKNYRY 530
 DB 481 QAKYLGILNKGPFKNYRY 500

RESULT 10
 ADO43989
 ID ADO43989 standard; protein; 597 AA.
 AC ADO43989;
 DT 15-JUL-2004 (first entry)

DE Amino acid sequence of human putative S-adenosylhomocysteinease.
 XX
 XX protein complex; neurological disease; stroke; neurodegeneration;
 XX Wallerian degeneration; Alzheimer's disease; neurological disorder;
 XX epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;
 XX atherosclerosis; ID-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2;
 KM ASK3; CamKII beta; CamKII delta; CamKII gamma; casein kinase II alpha;

KM Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,
 KM FLJ14653 NT2RP2002252; FLJ10839 FEBRA2002429; HERC2;
 KM inositol polyphosphate-5-phosphatase; inositol-1; 4;
 KM 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;
 KM Nek3; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;
 KM Pushover; S-adenosylhomocysteinease;
 KM secretory carrier-associated membrane protein 2; surfactant locus protein 2;
 KM ubiquitin carboxyl terminal hydrolase 11;
 KM upstream regulatory element binding protein 1; Vartul;
 KM Werner's syndrome helicase interacting protein; WHIP;
 KM X-ray repair cross complementing protein 4.
 OS Homo sapiens.
 XX
 XX WO2004031242-A2.
 XX
 XX PD 15-APR-2004.
 XX
 XX PF 11-SEP-2003; 2003WO-EP010110.
 XX
 XX PR 12-SEP-2002; 2002EP-00020495.
 XX PR 12-SEP-2002; 2002EP-00020496.
 XX PR 12-SEP-2002; 2002EP-00020497.
 XX
 XX (CELL-) CELLZONE AG.
 XX
 XX Boumeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;
 XX Kuester B, Hopf C;
 XX WPI: 2004-316467/29.
 XX
 XX New complex comprising at least one first protein, and at least one
 PT second protein, useful for treating stroke, Alzheimer's disease,
 PT neurological disorders such as epilepsy, and inflammatory conditions such
 PT as ulcerative colitis.
 XX
 XX Example, Page 191-193; 287pp; English.
 XX
 XX The specification describes protein complexes involved in cellular
 CC processes which have been shown to be critical for the development of
 CC various forms of neurological diseases. Three protein complexes were
 CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3
 CC protein complex. The protein complex are useful for treating diseases and
 CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,
 CC Alzheimer's disease, neurological disorders such as epilepsy, and
 CC inflammatory conditions such as ulcerative colitis, Crohn's disease or
 CC atherosclerosis. Proteins identified as being part of the protein
 CC complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,
 CC ASK1, ASK2, ASK3, CAMKII beta, CAMKII delta, CAMKII gamma, casein kinase
 CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,
 CC FLJ14653 NT2RP2002252, FLJ10839 FEBRA2002429, HERC2, two hypothetical
 CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,
 CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441,
 CC MSTP030, Nek3, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1
 CC precursor, Pushover, a putative S-adenosylhomocysteinease, secretory
 CC carrier-associated membrane protein 2, surfactant locus protein 2, ubiquitin
 CC carboxyl terminal hydrolase 11, upstream regulatory element binding
 CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),
 CC X-ray repair cross complementing protein 4 (isoform 1). The present
 CC sequence represents putative S-adenosylhomocysteinease.
 XX
 XX Sequence 597 AA;

Query Match 92.8%; Score 2582; DB 8; Length 597;
 Best Local Similarity 88.8%; Pred. No. 8, 1e-248;
 Matches 502; Conservative 8; Mismatches 19; Indels 36; Gaps 4;

QY 1 MSMPDMPDP-----GYGE--ELKQAKETEDAKKISFMAITVTKAPKK----- 40
 DB 34 ISQP-ALPLPDPDTPAPSGESENLRNLRQGRRAESSQNLRLRLVSAQNGRSDWRMLWI 92
 QY 41 -----QIQPADMQBFTKPTPTKGRSLSRSSISQSTDSYSSAASYTDS 85

DB 93 QLMPIIDSLIEISCFIQIQPADMQBFTKPTPTKGRSLSRSSISQSTDSYSSAASYTDS 152
 QY 86 DDEVSPPREKQNTNSKSSNFCVKNIKQAEFGRRREIEIAEQDMSALISLRKRAQGEKPLAG 145
 DB 153 DDEVSPPREKQNTNSKSSNFCVKNIKQAEFGRRREIEIAEQDMSALISLRKRAQGEKPLAG 212
 QY 146 AKIVCTHTIQTAVLIETLCALGACQCRWSACNISTONEVAALAEAGVAFPAKGESE 205
 DB 213 AKIVCTHTIQTAVLIETLCALGACQCRWSACNISTONEVAALAEAGVAFPAKGESE 272
 QY 206 DDFWMCIDRCVNMDDQANMILDDGGDLTHWYKKYPNVFKIRGIVEESVTGVRLYOL 265
 DB 273 DDFWMCIDRCVNMDDQANMILDDGGDLTHWYKKYPNVFKIRGIVEESVTGVRLYOL 332
 QY 266 SKAGKLCVPANMNVDSYTKQKFDNLVCCRESILDLGKRTTDMVFGQKVYGVGEVKG 325
 DB 333 SKAGKLCVPANMNVDSYTKQKFDNLVCCRESILDLGKRTTDMVFGQKVYGVGEVKG 392
 QY 326 CCAALKAALGAIYYTIEIDPICLQACMDGFRVVKLNEVIROVDVITCTGNKNVYTRHL 385
 DB 333 CCAALKAALGAIYYTIEIDPICLQACMDGFRVVKLNEVIROVDVITCTGNKNVYTRHL 452
 QY 386 DMRKNSCIVCMNGHSNTEIDVTSLTPELTWERVRSQYDHYVIMPDGKRVLLAEGRLNLT 445
 DB 453 DMRKNSCIVCMNGHSNTEIDVTSLTPELTWERVRSQYDHYVIMPDGKRVLLAEGRLNLT 512
 QY 446 SCSTVPPTFLVSTATTQALALIELVNAPEGRYKQDVLLPKKMDYVASLHLPSTDAHIT 505
 DB 513 SCSTVPPTFLVSTATTQALALIELVNAPEGRYKQDVLLPKKMDYVASLHLPSTDAHIT 572
 QY 506 ELTDDQAKYGLGNKGPFPKPNYRY 530
 DB 573 ELTDDQAKYGLGNKGPFPKPNYRY 597

RESULT 11

ABM60935
 ID ABM60935 standard; protein, 611 AA.

AC ABM60935;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) polypeptide PRO81608, SEQ:2410.

XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;

KW tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW cervical cancer; melanoma; leukaemia; hybridisation probe;

KW gene therapy; cytostatic.

OS Homo sapiens.

PN WO2004030615-A2.

PD 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.

PR 02-OCT-2002; 2002US-0414971P.

PA (GETH) GENENTECH INC.

PI Wu TD, Zhang Z, Zhou Y;

DR WPI: 2004-347921/32.

XX N-PSDB; ACN38718.

PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or

FT prostate cancer or tumor.

XX Claim 12; SEQ ID NO 2410; 7273bp; English.

CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX

XX Sequence 611 AA;

Query Match 88.3%; Score 2456; DB 8; Length 611;

Best Local Similarity 84.9%; Pred. No. 3.2e-235;

Matches 468; Conservative 31; Mismatches 24; Indels 28; Gaps 3;

QY 8 PLPGVGE-----ELKQAKEIEDAEKY-----SFMATVTKAP---K 39
DB 61 FVPGGSGPAAALSPAAGKVPQASAMKSDPHHQHRRHGDGEALVSPDGTVEAPRTVK 120
QY 40 KOIQPADMOEFTKPTKTGRSLRSISQSTDSYSSAASYTSSDDEVSREKQONS 99
DB 121 KOIQPADKQENKPKTKIGRSLRSISQSTDSYSSAASYTSSDDEVSREKQONS 180
QY 100 KSSSFCVKNIKQAEFGREIEIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAOTA 159
DB 181 KSSSFCVKNIKQAEFGREIEIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAOTA 240
QY 160 VLIETLALGAOCRWASACNIYSTONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNM 219
DB 241 VLMETLALGAOCRWACNIYSTONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNM 300
QY 220 GWOANMILDDGGDLTHWYKKYKPNVFKKIRGIVEESVTGVHRLYOLSKAGKLCVPAWNVN 279
DB 301 GWOANMILDDGGDLTHWYKKYKPNVFKKIRGIVEESVTGVHRLYOLSKAGKLCVPAWNVN 360
QY 280 DSVTKQKFDNLVCCRESILDDGLKRTTDMVFGGKQVAVCGYGEVGGCCALKALGAIYVI 339
DB 361 DSVTKQKFDNLVCCRESILDDGLKRTTDMVFGGKQVAVCGYGEVGGCCALKALGAIYVI 420
QY 340 TEIDICALQACMDQFRVYKLVNEVIROYDVVITCTGNXNVVTRHLDKRNKSCIVCNMGH 399
DB 421 TEIDICALQACMDQFRVYKLVNEVIROYDVVITCTGNXNVVTRHLDKRNKSCIVCNMGH 480
QY 400 SNTIEDVTSLSRTPETLWTRVRSQVHVITPDGKRVLLAEGRLNLSGTYVTFVLSTIA 459
DB 481 SNTIEDVTSLSRTPETLWTRVRSQVHVITPDGKRVLLAEGRLNLSGTYVTFVLSTIA 540
QY 460 TTOALALIELVNAPEGRYKODVYLLPKKQDEYVASLHPSFDAHTTELTDDQAKYLGANK 519
DB 541 TTOALALIELVNAPEGRYKODVYLLPKKQDEYVASLHPSFDAHTTELTDDQAKYLGANK 600
QY 520 NGPEKPNYRY 530
DB 601 NGPEKPNYRY 611

RESULT 12

ADSI0638
ID ADSI0638 standard; protein; 508 AA.

XX AC ADSI0638;

XX DT 16-DEC-2004 (first entry)

XX DE Human therapeutic protein - SEQ ID 875.

XX antiinflammatory; neuroprotective; antinaemic; cytostatic; vulnerary;
XX inflammatory; haematopoietic; immunity; neurodegenerative; stem cell;
XX aplastic anaemia; cancer; wound healing; gene therapy.

XX Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NIVE-) NIVELO INC.

XX Tang YF, Asundi V, Ren F, Zhang J, Wehman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AU, Weng G, Zhou P;

XX WPI; 2004-668857/65.

XX N-PSDB; ADS09954.

XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.

XX Claim 20; SEQ ID NO 875; 718bp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antinaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
XX disorders, such as aplastic anaemia or cancer, as well as for promoting
XX wound healing. The molecules may also be utilised during gene therapy
XX procedures. The current sequence is that of a human therapeutic protein
XX of the invention. The current sequence is not shown explicitly within the
XX specification but can be accessed from the WIPO web-site.

XX Sequence 508 AA;

Query Match 87.3%; Score 2429; DB 8; Length 508;

Best Local Similarity 92.1%; Pred. No. 1.2e-235;

Matches 454; Conservative 23; Mismatches 16; Indels 0; Gaps 0;

QY 38 PKQIQPADMOEFTKPTKTGRSLRSISQSTDSYSSAASYTSSDDEVSREKQOT 97
DB 16 PEMMIQFADQKQENKPKTKIGRSLRSISQSTDSYSSAASYTSSDDEVSREKQOT 75
QY 98 NSKSSNFCVKNIKQAEFGREIEIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAO 157
DB 76 NSKSSNFCVKNIKQAEFGREIEIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAO 135
QY 158 TAVLIETLALGAOCRWASACNIYSTONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVN 217
DB 136 TAVLIETLALGAOCRWACNIYSTONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVN 195
QY 218 MDGQANMILDDGGDLTHWYKKYKPNVFKKIRGIVEESVTGVHRLYOLSKAGKLCVPAWNVN 277
DB 196 VEGWQPNMILDDGGDLTHWYKKYKPNVFKKIRGIVEESVTGVHRLYOLSKAGKLCVPAWNVN 255
QY 278 VNSDVTKQKFDNLVCCRESILDDGLKRTTDMVFGGKQVAVCGYGEVGGCCALKALGAIY 337
DB 256 VNSDVTKQKFDNLVCCRESILDDGLKRTTDMVFGGKQVAVCGYGEVGGCCALKALGAIY 315

	Homo sapiens.
XX	MOZ00264795-A2.
PN	
PD	22-AUG-2002.
PF	
PE	08-FEB-2002; 2002WO-US003814.
XX	
PR	09-FEB-2001; 2001US-0268113P.
PR	15-FEB-2001; 2001US-0269215P.
PR	27-FEB-2001; 2001US-0272271P.
PR	07-MAR-2001; 2001US-0274091P.
PR	09-MAR-2001; 2001US-0274423P.
PR	23-MAR-2001; 2001US-0278479P.
PR	23-MAR-2001; 2001US-0278480P.
XX	
PA	(INCY-) INCYTE GENOMICS INC.
XX	
P1	Sanjanwala MM, Lu Y, Lee EA, Hafalia AJA, Warren BA, Baughn MK;
P1	Tang TY, Yue H, Yao MG, Lee S, Thornton M, Waila NK, Xu Y;
P1	Tren UK, Lal PG, Lu DAM, Swarnaker A, Jones KA, Ring HZ;
XX	
DR	WPI: 2002-643488/69.
DR	N-PDSB; ABK91312.
PT	New isolated human enzymes (NZMS), useful for diagnosing, treating and preventing immune system, developmental, eye, metabolic, smooth muscle, neurological, pulmonary and cardiac disorders, cancer, or parasitic infections.
PT	
PS	Claim 1; Page 147-149; 170pp; English.
XX	
CC	The invention relates to a new isolated human enzyme (NZMS) (I) and the encoding nucleic acid (II). The polypeptides and polynucleotides are useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of NZMS. The NZMS or its fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptide, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The antibody is useful in diagnosing a condition or disease associated with the decreased expression or overexpression of NZMS and in detecting (II). (I) is useful in the production of antibodies. The microarray is useful in monitoring or measuring gene expression profiles. The polypeptides and polynucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overexpression of NZMS, such as immune system disorders (e.g. acquired immune deficiency syndrome (AIDS), contact dermatitis), immune deficiencies (e.g. common variable immunodeficiency, Chediak-Higashi syndrome), developmental disorders (e.g. Cushing's syndrome, hypothyroidism), eye disorders (e.g. glaucoma, cataract), metabolic disorders (e.g. cystic fibrosis, sickle-cell anemia), smooth muscle disorders (e.g. asthma, lactic acidosis), neurological disorders (e.g. Parkinson's disease, epilepsy), cardiac disorders (e.g. congestive heart failure, myocardial infarction), pulmonary disorders (emphysema, bronchitis), parasitic infections (amoebiasis, filariasis), and cell proliferative disorders (e.g. cancer, leukemia). The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles. The present sequence represents the amino acid sequence of one of 11 novel human enzymes (NZMS1-11) of the invention
CC	
CC	
SQ	Sequence 564 AA;
	Query Match 87.3%; Score 2429; DB 5; Length 564;
	Best Local Similarity 90.3%; Pzed. No. 1.4e-232;
	Matches 455; Conservative 24; Mismatch 0; Gaps 0;
OY	
D6	
	27 KYSEFATYTKAPKKIOFADDDMQEFPKPTTKTGRSLSSISQSSSTDSYSASAYTSDSD 86
	61 KKXIVVNGNSGICAKIQIFDQKOEFKRRTKIGRSLSSISQSSSTDSSSAASTDDSD 120
OY	87 DEVSPREKQQTNSKSSSNFCVNKNIQAEFGREIEITAEODMSALISLRRAQGEKPLAGA 146

Db	12	DBTSRDRDQKQKSKSSSPFCVKNIKQAEFRGRREIEAEOEPMALMLARKBAQCEKPLAGA	180
Qy	147	KIVGCTHTTTAQTAVLIEITLCLGACQCRKSNCTISTONEVAAAALAEAGVAVPMKGESED	206
Db	181	KIVGCTHTTTAQTAVLIEITLCLGACQCRWAACNIYSTUNEVAAAALAEAGFPVPMKGESED	240
Qy	207	DFWMCIDCQVNMDDGQAMNLLDDGGDLTHWVYKXYPNVFPFKIRGIVESVTGVHRLYQLS	266
Db	241	DFWMCIDRCVNVBEGQPMNLLDDGGDLTHWYKXYPMFPFKIKGIVESVTGVHRLYQLS	300
Qy	267	KAGKLCVPMNVNVSVTQKQFENDLYCCRESILDLGKRTDVMFEGQVVCYGEVQKGC	326
Db	301	KAGKLCVPMNVNVSVTQKQFENDLYCCRESILDLGKRTDVMFEGQVVCYGEVQKGC	360
Qy	327	CAALKALGAIYITTEIDPICALQACMGDFRVKLNIEVIRQVDVYITCTGKNVVTREHLD	386
Db	361	CAALKAMGSIYVVEIDPICALQACMGDFRVKLNIEVIRQVDVYITCTGKNVVTREHLD	420
Qy	387	RKMSCIYCNMGHSTETEDVTSLSRTPELTWERVBSQVDHYIWPDKRVLLAEGRLNLNS	446
Db	421	RKMSCIYCNMGHSTETEDVTSLSRTPELTWERVBSQVDHYIWPDKRIVLLAEGRLNLNS	480
Qy	447	CSTVTFVLSITATTQALALIELYNAPBGRYKQDVLLPKKMDYVASLHLPSTDAHLTE	506
Db	481	CSTVTFVLSITATTQALALIELYNAPBGRYKQDVLLPKKMDYVASLHLPSTDAHLTE	540
Qy	507	LTFDDQAKYIGLNKNGPFKNYTRY 530	
Db	541	LTFDDQAKYIGLNKNGPFKNYTRY 564	
RESULT 15			
AC	ABBS8663	standard; protein; 521 AA.	
DT	ABBS8663;		
DT	26-MAR-2002 (first entry)		
DE	Drosophila melanogaster polypeptide SEQ ID NO 2781.		
DE	Drosophila; developmental biology; cell signalling; insecticide;		
XX	pharmaceutical.		
XX	Drosophila melanogaster.		
OS	WO200171042-A2.		
PN	27-SEP-2001.		
PD	23-MAR-2001; 2001WO-US009231.		
XX	23-MAR-2000; 2000US-0191637P.		
PR	11-JUL-2000; 2000US-00614150.		
XX	(PEKE) PE CORP NY.		
PA	Venter JC, Adams M, Li PMD, Myers EW;		
PI	WPI, 2001-656860/75.		
XX	N-PSDB; ABL02766.		
DR			
PT	New isolated nucleic acid detection reagent for detecting 1000 or more		
XX	genes from Drosophila and for elucidating cell signalling and cell-cell		
XX	interactions.		
XX	Disclosure; SEQ ID NO 2781; 21pp + Sequence Listing; English.		
XX	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		

CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB16175) and the encoded proteins (AAB57737-
CC AAB572072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
CY

Sequence 521 AA;

Sequence 521 AA;

Query Match	Score	DB 4	Length
70.8%	1970	521	

Best Local Similarity 77.6%; Pred. No. 7.8e-187;

Matches 370; Conservative 48; Mismatches 55; Indels 4; Gaps 3;

Qy	5	KIGRRLSSLSIGSSSTSDVSSSAASTYDSD--DEUSPREKOOTNSKXSSNNCKNI-KOA	113
Db	46	KKTSRRSRSSLSASSTDSFSS--ASTIGSESDGDVPPREKQKSKSGSSDFCVNITAGH	104
Qy	114	EFGREIEIEAEDMSALISLRRAOGEKPLAGAKIVGCTHTTAOTAVILEPLCALGAOCR	173
Db	105	AFGRREIEIEAEDMGPIILMKRRAEDKPLKDAKIVGCTHTINAOTAVILEPLVETGASVR	164
Qy	174	WASCNITSTQNEVAAALAAAGVAVVPAAMKGESEDDPWNCIDBCVNMMDGMAMMILDDGDL	233
Db	165	WACNITSTQNEVAAALAAAGSIPIPAMRETEEDPMWCIDBCVNAEWMQPMMLDDSGDA	224
Qy	234	THAVYKKTYPNVEFKIRGIVEESVTGWHRLYOLSKAGKLCVPAAMVNDSTVKQFEDNYLCC	293
Db	225	THMLKKYITPMKLYKGIYESVTGVHRLYOLSKAGKLTVPAMVNDSTVKTFEDNYLSC	284
Qy	294	RESILDGLKRTDVMFGKQVAVVCGIYGVKGCCKCALKALGAIYITTEIDPICALQACMD	353
Db	285	KESILDPLKRTDVMFGKQVAVVCGIDVGKGCALKGOGCIYITTEIDPICALQASMD	344
Qy	354	GFVYVVLNIEYIQOVAVITCTGNKNVYVRREHLDRKQNSCIYCMNGHSTELDTVLSLTP	413
Db	345	GFVYVVLNIEYIRVDTLVATATGNKNVYVREHMDKKKSGCIYCMNGHSTELDTVNGLTRPD	404
Qy	414	LTWERVRSQVDHVIWDEGRVVLLEBGRLLNCSGTEVPFLVLSITATTAATQALALIELYNAP	473
Db	405	LWEKRSQVDHVIWDEKGIYLLLEGRLVNCSGSIPIFAVISTATQALALIELFNAP	464
Qy	474	BGGYKQDVYLLPEKMDVEYASLHLSPPAHILTELTDQAKTLGINKGPFKNPYRY	530
Db	465	PGYKSKDVYLLPEPKMDVEYASLHLPLPDHILTELSDEQAKTGMINKGPFKNPYRY	521

Search completed: September 6, 2006, 19:21:42
Job time : 212.543 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:22:08 ; Search time 35.1413 Seconds
(without alignments)
1451.138 Million cell updates/sec

Title: US-10-683-610-1
Perfect score: 2781
Sequence: 1 MSMDAMPRLPGVGEELKQAK.....OAKYLGLKNGPFRKNRYRY 530

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2582	92.8	597	2	T08681
2	1781.5	64.1	527	1	S01302
3	1184.5	42.6	433	1	JC2480
4	1156	41.6	432	1	A26583
5	1146	41.2	432	1	A43629
6	1142	41.1	466	2	Af2580
7	1142	41.1	466	2	D97362
8	1141	41.0	437	2	T32918
9	1130	40.6	437	1	A45569
10	1129	40.6	433	2	T40763
11	1121.5	40.3	481	2	AG3505
12	1110	39.9	485	2	S38379
13	1108.5	39.9	430	1	A27655
14	1108	39.8	485	2	C71400
15	1106	39.8	463	2	H87280
16	1105	39.7	449	2	S50546
17	1104	39.7	485	2	S71621
18	1103	39.7	485	2	T06764
19	1078.5	38.8	462	1	H83591
20	1072.5	38.6	462	1	A46035
21	1072	38.5	479	1	A54040
22	1052.5	37.8	495	2	B70593
23	1040.5	37.4	492	2	D87005
24	1026	36.9	446	2	D82730
25	790.5	28.4	399	2	B72649
26	772.5	27.8	417	2	S58193
27	772.5	27.8	442	2	C90224
28	739	26.6	416	2	E70401
29	709	25.5	425	2	S75518

30	692	24.9	415	1	C64473	adenosylhomocysteine
31	690	24.8	425	2	AC1983	adenosylhomocysteine
32	684.5	24.6	417	2	F69085	adenosylhomocysteine
33	674.5	24.3	422	2	B75064	adenosylhomocysteine
34	674	24.2	405	2	G69499	adenosylhomocysteine
35	672.5	24.2	425	2	H71167	probable S-adenosyl
36	611.5	22.0	404	2	B72409	adenosylhomocysteine
37	598.5	21.5	427	2	G84375	adenosylhomocysteine
38	553	19.9	227	2	T15035	adenosylhomocysteine
39	275	9.9	120	2	S22958	adenosylhomocysteine
40	237.5	8.5	326	2	F69360	adenosylhomocysteine
41	135.5	4.9	324	2	D97262	probable phosphogly
42	127.5	4.6	641	2	C82206	methy1-accepting c
43	121.5	4.4	515	2	T40809	glutanyl-tRNA redu
44	116	4.2	409	2	C82072	D-3-phosphoglyceta
45	113	4.1	1506	2	T30886	Integumentary muc1

ALIGNMENTS

RESULT 1									
T08681									
adenosylhomocysteinease (EC 3.3.1.1) DKFZp564A1523 - human (fragment)									
N.Alternate names: protein DKFZp564A1523.1									
C.Species: Homo sapiens (man)									
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004									
C.Accession: T08681									
R.Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.									
submitted to the Protein Sequence Database, May 1999									
A.Reference number: Z16469									
A.Accession: T08681									
A.Molecule type: mRNA									
A.Residues: 1-597 <MAN>									
A.Cross-references: UNIPROT:Q9UG84; UNIPARC:UPI000006FAA4; EMBL:AL049954									
A.Experimental source: fetal brain; clone DKFZp564A1523									
C.Genetics:									
A.Note: DKFZp564A1523.1									
C.Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type									
C.Keywords: NAD; thioether hydrolase									
F.379-408/Region: beta-alpha-beta NAD nucleotide-binding fold									
F.244,278/Active site: Cys #status predicted									
Query Match									
Best Local Similarity 92.8%; Score 2582; DB 2; Length 597;									
Matches 502; Conservative 8; Mismatches 19; Indels 36; Gaps 4;									
OY	1	MSMDAMPRLP-----GVGE---ELKQAKELIDAEKYSFMATVTKAPKK-----	40						
DB	34	ISOP-ALPLPQETAPFGESLENLNRKQGRRAESSQNLISRLVSAQNGRSDMRWMI	92						
OY	41	-----OIQFADDMQEFKFPPTKGRSLRSISQSSSTDSYSSAASYDSS	85						
DB	93	QLWEIDSLSEISCLQIQFADDMQEFKFPPTKGRSLRSISQSSSTDSYSSAASYDSS	152						
OY	86	DDEVSPREKQQTNSGSSNFCVKNIKQAEFGRRRIETAEQMSALISIRKKAQGEKPLAG	145						
DB	153	DDEVSPREKQQTNSGSSNFCVKNIKQAEFGRRRIETAEQMSALISIRKKAQGEKPLAG	212						
OY	146	AKIVGCHTITQOTVLIETLALGAOCRWASACNISTONEVAALAEAGVAVFWAKGSE	205						
DB	213	AKIVGCHTITQOTVLIETLALGAOCRWASACNISTONEVAALAEAGVAVFWAKGSE	272						
OY	206	DDFWICIDRCVNDMGQAMNLLDDGDLTHWVYKYPNVFKIRIGIVEESTVGHRLYQL	265						
DB	273	DDFWICIDRCVNDMGQAMNLLDDGDLTHWVYKYPNVFKIRIGIVEESTVGHRLYQL	332						
OY	266	SKAKLTCVPANVNDSTYTKQFEDLYCCRESILDLGKRTTVMGGRQVYVCGVGEVKG	325						
DB	333	SKAKLTCVPANVNDSTYTKQFEDLYCCRESILDLGKRTTVMGGRQVYVCGVGEVKG	392						
OY	326	CCALKALGAIIVYTEIDPICALQACMDGFRVVKLNEVIRQVDVITCTGKNVVTREHL	385						

Db 393 CCAALKALGAIVYTEIDPICALQACMDGFRVVKLNEVIRQDVVITCTGNKVVTRHL 452

Qy 386 DRMKNSCIVCNMGHSNTEIDVTSLTPELTWERVRSQVDHVIMPDGKRVLLAEGRLLNL 445

Db 453 DRMKNSCIVCNMGHSNTEIDVTSLTPELTWERVRSQVDHVIMPDGKRVLLAEGRLLNL 512

Qy 446 SCSTVPFVLSTATTATQALALIELYNAPBGRYKQDVYLLPKKMDDEVASLHLPSPDAHLT 505

Db 513 SCSTVPFVLSTATTATQALALIELYNAPBGRYKQDVYLLPKKMDDEVASLHLPSPDAHLT 572

Qy 506 ELTDDQAKYLGKHNKRPFKNNYRY 530

Db 573 ELTDDQAKYLGKHNKRPFKNNYRY 597

RESULT 2

S01302

adenosylhomocysteinease (EC 3.3.1.1) - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: S01302

R/DeJorenzi, M.; Ali, N.; Saari, G.; Henry, C.; Wilcox, M.; Blenz, M.

EMBO J. 7, 3223-3231, 1988

A/Title: Evidence that the Abdominal-B r element function is conferred by a trans-regula

A/Reference number: S01302; MUID:89030618; PMID:2903049

A/Accession: S01302

A/Molecule type: DNA

A/Residues: 1-527 <DEL>

A/Cross-references: UNIPROT:P50245; UNIPARC:UPI000016B80E; EMBL:X13166; NID:g7675; PIDN:

C/GeneticS:

A/Gene: FlyBase:Abd-B

A/Cross-references: FlyBase:FBgn0000015

A/Intons: 17/3; 41/1; 263/2; 369/3; 451/1

C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type

C/Keywords: NAD; thioether hydrolase

F/275-304/Region: beta-alpha-beta NAD nucleotide-binding fold

F/140,114/Active site: Cys #status predicted

Query Match 64.1%; Score 1781.5; DB 1; Length 527;

Best Local Similarity 70.8%; Pred. No. 3.1e-130;

Matches 328; Conservative 64; Mismatches 68; Indels 3; Gaps 3;

Qy 64 SRISQSSSTDSYSSAASYTSDSDDE-VSPREKQOTNSKSSNFCYKNTKQAEFGREIEI 122

Db 27 ARFSDVSTCSFSSTYC-FTGSSDEBDVSPKDNHONRSAGTDFCVKSSISKAFGRREIEI 85

Qy 123 AEQMSALISLRKROGKEPLAGAKIVGCTHTTAOTAVLIENTLCAAGCRRASACNIYST 182

Db 86 ABSEPMGIMTLKRAKDEKPLKANIIGCTHYNAQSAVLIELVQLGATVRMAACNIYST 145

Qy 183 QNEVAALAEAGVAVFAMKGESEDDFWMCIDRCVMMDGWQANMILDDGGDLTHWYKKYP 242

Db 146 QNAVAALAEAGIPIFAVRGETEEFPMWCLDRAIYSDGWQRLILDDGGDATHLMLKKYP 205

Qy 243 NVFKKIRIGIVESTVGVHRLYOLSKAGKLCVPAWNVDSVTQKQDNLYCCESLIDGLK 302

Db 206 DYFAKIRIGIVESTVGVHRLYMLSKGKGLTPAIVNDSVTNKKPDTFTCRDSTILDSLK 265

Qy 303 RTTDMFGSKOVVVCYGEVGGCCALKALGAIYITEIDPICALQACMDGFRVVKLNE 362

Db 266 RTTDMFGSKOVVVCYGEVGGCCALKALGAIYITEIDPICALQACMDGFRVVKLNE 325

Qy 363 VIRQDVVITCTGNKVVTRHLDRMKNSCIVCNMGHSNTEIDVTSLTPELTWERVRSQ 422

Db 326 VIRQDVVITCTGNKVVTRHDMRMKNSCIVCNMGHSNTEIDVTSLTPELTWERVRSQ 385

Qy 423 VDHVIMPDGKRVLLAEGRLLNLSCSTVPFVLSTATTATQALALIELYNAPBGRYKQDV 482

Db 386 VDHVIMPDGKRVLLAEGRLLNLSCSTVPFVLSTATTATQALALIELYSPAR-GRYKSDVY 444

Qy 483 LLPKMDDEVASLHLPSPDAHLTELTDQAKYLGKHNKRPFK 525

Db 445 LLPKMDDEVASLHLPSPDAHLTELTDQAKYLGKHNKRPFK 487

RESULT 3

JC2480

adenosylhomocysteinease (EC 3.3.1.1) - African clawed frog

N/Alternate names: S-adenosyl-L-homocysteine hydrolase

C/Species: Xenopus laevis (African clawed frog)

C/Date: 29-Mar-1995 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C/Accession: JC2480

R/Seery, L.T.; McCabe, B.D.; Schoenberg, D.R.; Whitehead, A.S.

Biochem. Biophys. Res. Commun. 205, 1539-1546, 1994

A/Title: S-Adenosyl-L-homocysteine hydrolase from Xenopus laevis: Identification, developm

A/Reference number: JC2480; MUID:95110290; PMID:7811234

A/Accession: JC2480

A/Molecule type: mRNA

A/Residues: 1-433 <SEB>

A/Cross-references: UNIPROT:P51893; UNIPARC:UPI00001354E1; GB:L35559; NID:g558507; PIDN:

A/Experimental source: liver

C/Function:

A/Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adeno

C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type

C/Keywords: NAD; thioether hydrolase

F/215-244/Region: beta-alpha-beta NAD nucleotide-binding fold

F/79,113/Active site: Cys #status predicted

Query Match 42.6%; Score 1184.5; DB 1; Length 433;

Best Local Similarity 52.9%; Pred. No. 5e-84;

Matches 227; Conservative 81; Mismatches 118; Indels 3; Gaps 3;

Qy 104 NFCVNIQKQAEFGREIEIAQODMSALISLRKROGKEPLAGAKIVGCTHTTAOTAVLIE 163

Db 6 SYKVAADISLADWGRKALEIAENEMPGLMKXMEHSESRPLGAKIAGCLHMTLOTAVLIE 65

Qy 164 TLCAAGACRRASACNIYSTQNEVAALAEAGVAVFAMKGESEDDFWMCIDRCVNN-DGQ 222

Db 66 TLTHAGVAVQWSSCNIFSTQDHAALAKGVPAWAMGETDEEYIWCIEQIYFKDGKP 125

Qy 223 ANMILDDGGDLTHWYKKYPNVFVKIRIGIVESTVGVHRLYOLSKAGKLCVPAWNVDSV 282

Db 126 LNMILDDGGDLTHWYKKYPNVFVKIRIGIVESTVGVHRLYOLSKAGKLCVPAWNVDSV 185

Qy 283 TKQKFDNLYCRESLIDGKRTTDMFGSKOVVVCYGEVGGCCALKALGAIYITEI 342

Db 186 TKSKFDNLYCRESLIDGKRTTDMFGSKOVVVCYGEVGGCCALKALGAIYITEI 245

Qy 343 DPICALQACMDGFRVVKLNEVIRQDVVITCTGNKVVTRHLDRMKNSCIVCNMGHSNT 402

Db 246 DPINALQACMDGFRVVKLNEVIRQDVVITCTGNKVVTRHLDRMKNSCIVCNMGHSNT 305

Qy 403 EIDVTSLTPELTWERVRSQVDHVIMPDGKRVLLAEGRLLNLSCST-VPTFVLSTATT 461

Db 306 ELDVYMLNENAVKKNIPQVDRYLLKNGRHILLAEGRLLNLSCSTVPTFVLSTATT 365

Qy 462 QALALIELYNAPBGRYKQDVYLLPKKMDDEVASLHLPSPDAHLTELTDQAKYLGKHNK 521

Db 366 QVMAQIELMTTDT-KYRPGVYFLPKKDEAVAAHLDTGKYLTLTKQAKYLGKHNK 424

Qy 522 PFKNNYRY 530

Db 425 PFKNNYRY 433

RESULT 4

A26583

adenosylhomocysteinease (EC 3.3.1.1) - rat

N/Alternate names: S-adenosyl-L-homocysteine hydrolase

C/Species: Rattus norvegicus (Norway rat)

C/Date: 19-Nov-1988 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C/Accession: A26583; A26191; B26191; S69333

R/Ogawa, H.; Gomi, T.; Mueckler, M.M.; Fujioaka, M.; Backlund Jr., P.S.; Aksemit, R.R.; Ur

Proc. Natl. Acad. Sci. U.S.A. 84, 719-723, 1987

A/Title: Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from rat liver as det

A/Reference number: A26583; MUID:87118240; PMID:3027698

submitted to the EMBL Data Library, January 1998
A:Description: The sequence of C. elegans cosmid K02F2.
A:Reference number: Z21246
A:Accession: J132918
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-437 <MAG>
A:Cross-references: UNIPROT:P27604; UNIPARC:UPI00001354EA; EMBL:AF043699; P1DN:AA097565.
R:Prasad, S.S.; Scart, T.V.; Rose, A.M.
Genome 36, 57-65, 1993
A:Title: Molecular characterization in the dby-14 region identifies the adenosylhomocysteine to adenosyl-L-homocysteine hydrolase, human SAHH type
A:Reference number: Z22017; MUID:93209535; PMID:8458573
A:Accession: T41749
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-437 <PRA>
A:Cross-references: UNIPARC:UPI00001354EA; EMBL:S57284; P1DN:AA025906.1
C:Genetics:
A:Gene: K02F2.2
A:Map position: 1
A:Insertions: 74/3; 326/3
C:Function:
A:Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adenosyl-L-homocysteine hydrolase, human SAHH type
C:Keywords: NAD; chioether hydrolase

Query Match 41.0%; Score 1141; DB 2; Length 437;
Best Local Similarity 52.4%; Pred. No. 1.2e-80;
Matches 225; Conservative 78; Mismatches 120; Indels 6; Gaps 4;

Qy 107 VKNIKQAEFGREIEIAEDMSALISLRKAQGEKPLAGAKIVGCTHTTAQTAVLI 166
Db 10 VADIKLADFGKEIILENEMPGMLAMSKYGPSOPLGARIAGCLMHTITTAVALI 69
Qy 167 ALGAQCRWSACNISTONEVAALAEAGVAVFAMKGESEDDFWWCIDRCV--NMD 219
Db 70 ALGAQCRWSACNISTONEVAALAEAGVAVFAMKGESEDDFWWCIDRCV--NMD 219
Qy 226 ILDDGDLTHWVYKYPNVFKIRGIYVESVTVGHRLYQLSKAGLCVPAWNVDSVT 285
Db 130 ILDDGDLTHWVYKYPNVFKIRGIYVESVTVGHRLYQLSKAGLCVPAWNVDSVT 285
Qy 286 KFDNLVCCRSEILDLGKRTTDMFGKQVWVCGVEVGKGCALKAALGAVITTDPI 345
Db 190 KFDNLVCCRSEILDLGKRTTDMFGKQVWVCGVEVGKGCALKAALGAVITTDPI 345
Qy 346 CALQACNDGFRVVKLNEVIRQVDVITCTGNKNVYTRHLDKMKNSCIWNGHSHN 405
Db 250 CALQACNDGFRVVKLNEVIRQVDVITCTGNKNVYTRHLDKMKNSCIWNGHSHN 405
Qy 406 VTSLRPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSCST-VPTFVLSTAT 464
Db 310 VTSLRPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSCST-VPTFVLSTAT 464
Qy 465 ALILV---YNAPEGRYKQDVVLLPKMDRYVASLHLPSPDAHLELTDDQAKYIG 521
Db 370 AQLVLMWKFGTPQ-EYKLGIVLPLKTLDEEVAVLAQLGVKTKLSDQASVYGV 428
Qy 522 PFKPNYRY 530
Db 429 PFKPNYRY 437

RESULT 9
A45569
adenosylhomocysteinease (EC 3.3.1.1) - Leishmania donovani
N:Alternate names: S-adenosyl-L-homocysteine hydrolase
C:Species: Leishmania donovani
C:Date: 03-Feb-1994 #sequence_revision 04-Oct-1996 #text_change 15-Mar-2004
C:Accession: A45569
Mol. Blochem. Parasitol. 53, 169-183, 1992

A:Title: Cloning of the gene encoding Leishmania donovani S-adenosylhomocysteine hydrolase
A:Reference number: A45569; MUID:92365726; PMID:1501636
A:Accession: A45569
A:Molecule type: DNA
A:Residues: 1-437 <HEN>
A:Cross-references: UNIPARC:UPI0000172A02
A:Note: this sequence is inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:111168, NCBI:P111170)
C:Function:
A:Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adenosyl-L-homocysteine hydrolase, human SAHH type
C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
C:Keywords: NAD; chioether hydrolase
F:213-242/Region: beta-alpha-beta NAD nucleotide-binding fold
F:76,110/Active site: Cys #status predicted

Query Match 40.6%; Score 1130; DB 1; Length 437;
Best Local Similarity 52.2%; Pred. No. 8.6e-80;
Matches 228; Conservative 74; Mismatches 125; Indels 10; Gaps 5;

Qy 103 SNFCVKNIKQAEFGREIEIAEDMSALISLRKAQGEKPLAGAKIVGCTHTTAQTAVLI 162
Db 2 ADVIKKDISLAEWKRAIILENEMPGMLAEIRREYGPSOPLGAKIAGCLMHTVOTAVLI 61
Qy 163 ETLICALQCRWSACNISTONEVAALAEAGVAVFAMKGESEDDFWWCIDRCV--NMD 219
Db 62 ETLICALQCRWSACNISTONEVAALAEAGVAVFAMKGESEDDFWWCIDRCV--NMD 219
Qy 220 GWOANMILDDGDLTHWVYKYPNVFKIRGIYVESVTVGHRLYQLSKAGLCVPAWNV 279
Db 122 G-LPNNMILDDGDLTHWVYKYPNVFKIRGIYVESVTVGHRLYQLSKAGLCVPAWNV 180
Qy 280 DSVTKQKFDNLVCCRSEILDLGKRTTDMFGKQVWVCGVEVGKGCALKAALGAVIT 339
Db 181 DSVTKQKFDNLVCCRSEILDLGKRTTDMFGKQVWVCGVEVGKGCALKAALGAVIT 339
Qy 340 TELDIPICALQACNDGFRVVKLNEVIRQVDVITCTGNKNVYTRHLDKMKNSCIWNGH 399
Db 241 TELDIPICALQACNDGFRVVKLNEVIRQVDVITCTGNKNVYTRHLDKMKNSCIWNGH 399
Qy 400 SNTFIDVTSLRPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSC-STVPFVLSIT 458
Db 301 SNTFIDVTSLRPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSC-STVPFVLSIT 458
Qy 459 ATTOALILIELY-NAPEGRY---KQDVVLLPKMDRYVASLHLPSPDAHLELTDDQAK 513
Db 361 ATTOALILIELY-NAPEGRY---KQDVVLLPKMDRYVASLHLPSPDAHLELTDDQAK 513
Qy 514 YLGAKNGPFPKPNYRY 530
Db 421 YLGAKNGPFPKPNYRY 437

RESULT 10
T40763
adenosylhomocysteinease - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40763
R:Lyne, M.; Rajadream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.
submitted to the EMBL Data Library, March 1998
A:Reference number: Z21948
A:Accession: T40763
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-433 <LYN>
A:Cross-references: UNIPROT:O13639; UNIPARC:UPI000013550C; EMBL:AL022072; P1DN:CAA17833.1
A:Experimental source: strain 972h-; cosmid c8D2
C:Genetics:
A:Gene: SPDB:SPB08D2.18C
A:Map position: 2
C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type

Query Match 40.6%; Score 1129; DB 2; Length 433;

Best Local Similarity 50.7%; Pred. No. 1e-79; Matches 219; Conservative 81; Mismatches 128; Indels 4; Gaps 3;

QY 102 SSNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTAOTAVL 161
 Db 3 TQNYKADISLAFGKEIEIAENEMPGIIAVERKAKSQPLKARIACCLMHTIOTAVL 62
 QY 162 IETLCALGAQCRWSACNIYSTONEVAALAEAGVAVFANKGSEDDFWMCIDRCVNM--D 219
 Db 63 IETVLVGALEVWSSCNISTODHAAAAIAATGVPVFAWKGETEEBEYLICIQQLSPFS 122
 QY 220 GQOANMILLDDGGDLTHWVYKXYPNVFKIRGIVESVTGVHRLYQSKGKLCVPMANN 279
 Db 123 GRLNNMILLDDGGDLTALVHERHPELLVDIRGISEETTTVHNLKXKFKKXKLVPIVNN 182
 QY 280 DSVTKQKPNLYCCRESILDGKRTTDVWFGKQVAVCGYGVGKCCALKALGAIYI 339
 Db 183 DSVTKSKPNLYCCRESILDGKRTTDVWFGKQVAVCGYGVGKCCALKALGAIYI 242
 QY 340 TEIDPICALQACMDGFRVVKLVNEVIRQVDVITCTGNKQVAVTRELDRMKNSCIYCNMGH 399
 Db 243 TEVDPIALQACMDGFRVVKLVNEVIRQVDVITCTGNKQVAVTRELDRMKNSCIYCNMGH 302
 QY 400 SNTETDVSILRTEPTEWVERVRSQVDHVIWPDGRVVLAEGRLLNLSCT-VPTFVLSTI 458
 Db 303 FDEVIDVAVLWKNANQDVNIKQVDYELKNSHIIILLADGRLVNLGCAVYHPSEFVMSCS 362
 QY 459 ATTQALALIELYNADEGRYKQDVYLLPKKMEDEVASLHLPSPDAHLTELTDQAKYLGLN 518
 Db 363 FPNQVLAQIALW-TDNTSYPLGVHMLPKLDEBEVALHIGKLGVLKTLTITSVQSDVLGIP 421
 QY 519 KNGPKPKNYRY 530
 Db 422 VDGPKYKADHYRY 433

RESULT 11
 AG3505
 adenosylhomocysteinease (EC 3.3.1.1) (imported) - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Mar-2004
 C:Accession: AG3505
 R:DelVecchio, V.G.; Kaparatel, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova, J.; Mazur, M.; Goltzman, E.; Selikov, B.; Elser, P.H.; Hadjios, S.; O'Callaghan, D.; Telles, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AG3505
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-481 <KUR>
 A:Cross-references: UNIPARC:UPI00000582D0; GB:AE008917; PIDN:AAL53210.1; PID:g17984086;
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI2029
 A:Map position: I
 C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
 C:Keywords: chloether hydrolase

Query Match 40.3%; Score 1121.5; DB 2; Length 481;
 Best Local Similarity 48.6%; Pred. No. 4.5e-79;
 Matches 233; Conservative 75; Mismatches 124; Indels 47; Gaps 8;

QY 96 QTNKSG-----SSNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKI 148
 Db 6 QANCGLEHAMTASQDFVVKIDISLADWGRREDIAETEMPGIIMAAAREFGKSGQPLKARI 65
 QY 149 VECTHTTAOTAVLITLCLALGAQCRWSACNIYSTONEVAALAEAGVAVFANKGSEDDFW 208
 Db 66 SSLSHMTIOTAVLITLCLALGAQCRWSACNIYSTODHAAAAIAATGVPVFAVKGETLEY 125
 QY 209 WMCIDRCVNM-DGMOANMILLDDGGDLTHWV-----YKK 240

Db 126 WTYDQITQWMDGERSNNMILLDDGGDATMYIILGARAEGEDVLSNPQSEBEVLPFAQIK 185
 QY 241 ----YPNVEKK-----IRGIVESVTGVHRLYQLSXAGKLCVPMANNVDSVTKQKPNLYC 292
 Db 186 RMAARPGFFTKQRAIKGVTEETTTGVNRLYQLQKGLLPPPAIVNDSVTKSKFDNKYG 245
 QY 293 CRESILDLGKRTTDVWFGKQVAVCGYGVGKCCALKALGAIYIETIDPICALQAC 352
 Db 246 CKESLVDIRGRTDVMAGKVAVVCYGVDVGKSAQSLAGARVTEVDPICALQAM 305
 QY 353 DGFVRVVKLVNEVIRQVDVITCTGNKQVAVTRELDRMKNSCIYCNMGHNTETIDVTSRLTP 412
 Db 306 DGFVYVITLDDAASRTDIYVTTGKNDVITIDMRKMKMCIVGNIQHEDNEIQVALR-- 363
 QY 413 ELTWERVSQVDHVIWPDGRVVLAEGRLLNLSCT-VPTFVLSTIATQALALIELYN 471
 Db 364 NLKMTNVAPQVDLLEFPGRKRLILLSGRLLNLGATGHPSEFVMSASFTNOVLQOIELFT 423
 QY 472 APEGKQDVYLLPKKMEDEVASLHLPSPDAHLTELTDQAKYLGLNKGPFKPYRY 530
 Db 424 RTDA-YKNNEVYVLPRLHDEKVARLRLDLKGLKTLVLSEQAAYIGVTPQGPKSEHYRY 481

RESULT 12
 S38379
 adenosylhomocysteinease (EC 3.3.1.1) - Madagascari periwinkle
 N:Alternate names: S-adenosyl-L-homocysteine hydrolase
 C:Species: Catharanthus roseus (Madagascar periwinkle)
 C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S38379
 R:Schröder, G.; Waite, A.; Horze, M.; Schröder, J.
 Submitted to the EMBL Data Library, October 1993
 A:Description: cDNA for stress-induced S-adenosyl-L-homocysteine hydrolase from Madagascari
 A:Reference number: S38379
 A:Accession: S38379
 A:Molecule type: DNA
 A:Residues: 1-485 <SCH>
 A:Cross-references: UNIPROT:P35007; UNIPARC:UPI00001354EB; EMBL:Z26881; NID:ig407411; PID
 C:Genetics:
 A:Gene: SAHH
 C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
 C:Keywords: NAD; chloether hydrolase
 F:263-297/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:186/120/Active site: Cys #status predicted

Query Match 39.9%; Score 1110; DB 2; Length 485;
 Best Local Similarity 46.4%; Pred. No. 3.6e-78;
 Matches 224; Conservative 85; Mismatches 124; Indels 50; Gaps 8;

QY 95 QQTNKSGSSNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHI 154
 Db 6 EKTSS--GREYKVVDMSQADFGRLIEIAEVEEMGLMSCRAEFGSPQPKAKITGSLHM 63
 QY 155 TAOTAVLITLCLALGAQCRWSACNIYSTONEVAALAEAGVAVFANKGSEDDFWMCIDR 214
 Db 64 TITRAVLEITLALGAQCRWSACNIYSTODHAAAAIAADSAVFAWKGETIOEYVWCHE 123
 QY 215 CVNM--DGMOANMILLDDGGDLTHWYK----- 239
 Db 124 ALDWCPDG-GBDILVDDGDATLLIHGKVAEEYKNGALPDPSTDNAEFOIVLTIR 182
 QY 240 -----KYNVFKKIRGIVESVTGVHRLYQLSXAGKLCVPMANNVDSVTKQKPNLYC 291
 Db 183 DGLKSDPTKTYRMRERLVGSEETTTGVKRLYQOMANGTLLFPAINVDSVTKSKFEDLY 242
 QY 292 CRESILDLGKRTTDVWFGKQVAVCGYGVGKCCALKALGAIYIETIDPICALQAC 351
 Db 243 GGRSLPGLMARLADVWLAGVAVVAGVDVGKCCALKALGAIYIETIDPICALQAT 302
 QY 352 MDGFRVVKLVNEVIRQVDVITCTGNKQVAVTRELDRMKNSCIYCNMGHNTETIDVTSRLT 411
 Db 303 MEGQVLTLEDVVSADIPVTTTGNKDIINVDHMRKKNNAIVGNIQHEDNEIDMLGLET 362

RESULT 13

A27655
adenosylhomocysteinease (EC 3.3.1.1) - slime mold (*Dicystostelium discoideum*)
N/Aternate names: S-adenosyl-L-homocysteine hydrolase
C/Species: *Dicystostelium discoideum*
C/Date: 31-Mar-1989 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C/Accession: A27655; S06394
R/Kaestli, J.; Aksemit, R.R.; Backlund Jr., P.S.; Cantoni, G.L.
Biochem. Biophys. Res. Commun. 153, 359-364, 1988
A>Title: Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from *Dicystostelium d.*
A/Reference number: A27655; MUID:08240426; PMID:3288206
A/Accession: A27655
A/Molecule type: mRNA
A/Residues: 1-430 <XAS>
R/Gulton, M.C.; Part, D.; Veron, M.
Biochimie 70, 835-840, 1988
A>Title: Cloning of a cDNA for the S-adenosyl-L-homocysteine hydrolase from *Dicystostelium d.*
A/Reference number: S06394; MUID:09000991; PMID:3139100
A/Accession: S06394
A/Molecule type: mRNA
A/Residues: "VVTKSSWPKPELHYQT", 270-311, 'G', 313-323, 'S', 325-359, 'SVTK', 365-382, 'F', 384-430
A/Cross-references: UNIPARC:UPI000016B98D; EMBL:X12523; NID:g7204; PIDN:CA031040.1; PID:
A/Note: this sequence differs at the amino end by an apparent frame shift; comparison to C:/Function:
C:/Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adenosyl-L-homocysteine and methanethiol
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
C/Keywords: NAD; thioether hydrolase
E:213-242/Region: beta-alpha-beta NAD nucleotide-binding fold
E:78,112/Active site: Cys #status predicted

Query Match 39.9%; Score 1108.5; DB 1; Length 430;
Best Local Similarity 51.9%; Pred. No. 3.9e-78;
Matches 222; Conservative 72; Mismatches 131; Indels 3; Gaps 3;

Oy 104 NECVKNIKQAEFGRRREIEIEMODMSALISLRKRAQGEPLAGAKIVGCCHITPOTAVILE 163
Db 5 HKYKDVISLAAMRKKEIEIANEMPGLMTLEKKGPAPQILKARINAGCLAHMTIQTAVILLE 64
Oy 164 TLCAAGAOCRMASACNIYSTONEVAALAEAGVAAPAMGESSEDDPMWCICDRCNNDGWQA 223
Db 65 TLTALGAQOVQMSSCNIFSTDOQAALAATATVPAYAMGETEEENMCVEQTIIVFDGDGL 124
Oy 224 NMILLDGGDLTHWVYKYKPYNVFFKIRIGIVEESVTGVHRLYQLSKAGKLCPVPMNNVDSYT 283
Db 125 NMILLDGGDLTLVHEKYPQFLAGIKGISSETTHGVHLNYMKFKSGKLKVPAINNVDST 184
Oy 284 KQKFDNLVCCRESILDGLKRTTDVMFGQKVVVGCGYEVGKGCCAAALKALGAIYYITEID 343
Db 185 KKFDFNLVCCRSLIDGIKRATDVMIAGKVAVVAGYGDKGCAOSLSFMGARVYATEID 244
Oy 344 PLCALOACMDGFRFVLKLVNEVIROYDVITTCGNKKVYRREHLDPMKNSGITVCMGGSNTE 403
Db 245 PLNALOACMDGVQVITMETAAPLSNIFPTTGCRITVGEHNPAWKEDATVCNICGFDE 304
Oy 404 IDVTSRTPELTIERVRSQVDHVIMPDGKRVLVLAEGRLNLSGST-VPTFLSTATQ 462
Db 305 IDVAMVMA-NAKDDTVKRPQVDRIYLANGVHIILAEGRLVNLGCGTHGPSFMNSFCNQ 363
Oy 463 ALALLELVNAPEGRYKODVYLPRKKMEYVASLHPSDAHLTELTDQAKYLGINKGP 522

Db 364 TLAQALMTKTE-EKPLGVALPKLIDEEVARLHLOGLAKLTITTEKQSEYLSVPAAGP 422

Qy 523 FKENTYRY 530
: : : : :
Db 423 YKVDHYRY 430

RESULT 14

C71400
adenosylhomocysteine (EC 3.3.1.1) [similarity] - Arabidopsis thaliana
N.Alternate names: protein DL3010W; S-adenosyl-L-homocysteine hydrolase
C.Species: Arabidopsis thaliana (mouse-ear cress)
A.Variety: Columbia
C.Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004
C.Accession: C71400, I51608
R.Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks
P.; Wedler, H.; Wedler, E.; Mamut, R.; Weisenegger, T.; Pohl, T.M.; Terry, N.; Gietz
vanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Scheffer, M.; Funk, B.
Nucleotide 331, 485-488, 1998
A.Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech,
ehoff, A.; Moores, T.; Jones, J.D.G.; Enevas, T.; Palme, K.; Benes, V.; Reichen, S.; Anst
C.; Chalvatzis, N.
A.Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thaliana
A.Reference number: A71400; MUID:98121113; PMID:9461215
A.Accession: C71400
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-485 <BEV>
A.Cross-references: UNIPROT:023355; UNIPARC:UPI000000A82; GB:297335; NID:92244747; PIDN:
R.Belbahri, L.; Elieuch, H.; Villareel, R.; Inze, D.; Thomas, D.; Thomasset, B.
Plant Physiol. 121, 313, 1999
A.Title: The isolation of an Arabidopsis thaliana cDNA clone encoding S-adenosyl-L-homocys
A.Reference number: Z25409
A.Accession: T51608
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-485 <BEL>
A.Cross-references: UNIPARC:UPI000000A82; EMBL:AF059581; PIDN:AAC14714.1
A.Experimental source: cultivar Landsberg erecta
C.Genetics:
A.Gene: SAHH
A.Map position: 4COP9-4G3845
A.Note: DL3010W
C.Subfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
C.Keywords: NAD; thioether hydrolase
F.263-299/Region: beta-alpha-beta NAD nucleotide-binding fold
F.186,120/Active site: Cys #status predicted

Query Match 39.8%; Score 1108; DB 2; Length 485;
Best local Similarity 45.2%; Pred. No. 5, 1e-78;
Matches 218; Conservative 92; Mismatches 124; Indels 48; Gaps 7;

Qy 95 OQTNKSGSNFVCVKIKAKAFGRREIEIAEQMSALISLRKAQSGKPLAGAKIVGCTHI 154
: : : : :
Db 6 EKTSS--GREYKVKMSQADFGRLLELAELVEMPGIMACRTGEPGQPFKGAIITSSLHM 63
: : : : :
Qy 155 TAQTFVLLETICALGAQCRWSACNIYSTONEVAALAEAGVAVFAKNGSEDDPFWMCIDR 214
: : : : :
Db 64 TICTRVLLLETICALGAERWCSNIFSTODHAAALARSAAVFAKNGETLQGYWCTER 123
: : : : :
Qy 215 CVNM--DGMQANMILDDGSDLTHWY----- 238
: : : : :
Db 124 ALDMGPGGPDILVDGDDATLLIHGVAAKEIPEKTGVDPPTSTDNDEFOIVLSIIE 183
: : : : :
Qy 239 -----KTPNVFKKIRGIVESVYGVRHLYOLSKAGKLCVAMNNNDVTKKPNLYC 292
: : : : :
Db 184 GLQVDPKKYHKRKEKLVSEETTTGVKRLVYOMQONGTLTLPAINVNDSTYKSKFPNLYG 243
: : : : :
Qy 293 CRESITLDELKRTTDMVFGSKVYVCGYGVGKCCAAALKALGAIYVITEIDPICALQACM 352
: : : : :
Db 244 CRHSIPDLMARATDVMINGKVAIVICGYGDVGCAAAAKMTAGARIVITEIDPICALQALM 303
: : : : :

Search completed: September 6, 2006, 19:30:44
Job time : 37.1413 secs

```
QY 353 DGRVVKLNEVIRQDVVITCTGNKRVVTRHLDKMKNSCIYCNMGHSTELDVTSLRT- 411
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 304 EGIQVLTLEDVSEADIFVTTTGNKDIIIVDHRKKNNAIYCNIGHFNEIDMGLERY 363
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 412 PELTERVRSQVDHVIMPDGKR-VVLLAGRLNLNLSCT-VPTFVLSTATTQALALIEL 469
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 364 PGVKRTTIPQTDKRWVFPETKAGIIVLAGRLNLNLSCTVMSCSFTNOVIAQLEL 423
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 470 YN-APBGRYKQDVYLLPKMKDEVASLHLPSPDHALTELTDQAKYLGINKGPFKNY 528
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 424 MNEKASGKYEKKYVLPKHLDEKVALHLHGKLGARLTKLKSDQSDYVSIPIGPYKPHY 483
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 529 RY 530
      ||
Db 484 RY 485
```

RESULT 15

H87280

adenosylhomocysteinease [imported] - Caulobacter crescentus

C.Species: Caulobacter crescentus

C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C.Accession: H87280

R.Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A.Title: Complete Genome Sequence of Caulobacter crescentus.

A.Reference number: A87249; MUID:21173698; PMID:11259647

A.Accession: H87280

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-463 <STO>

A.Cross-references: UNIPROT:Q9ABH0; UNIPARC:UPI00001354BC; GB:AE005673; NID:G13421390; F

C.Genetics:

C.Superfamily: S-adenosyl-L-homocysteine hydrolase, human SMH type

C.Gene: CC0257

Query Match 39.8%; Score 1106; DB 2; Length 463;

Best Local Similarity 47.9%; Pred. No. 6.8e-78;

Matches 226; Conservative 82; Mismatches 110; Indels 54; Gaps 8;

```
QY 103 SNFCVKNIKQAEFRREIETIAEQDMALISLKRAGKEKPLAGAKIVGCTHITAOTAVLI 162
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 ADVIVKDISLADFGREIETIAETEMPGLATREYGPQOILKGARLAGSLHMTTOTAVALI 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 ETLTALGAQCRRWACNIYSTONEVAALAEAGVAVFAMKGESEDDFW-----WCIDR 214
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 ETLTALGAQVRWASCNIFSTQDHAAAIAAGVAVFPAFGENLVETWEYAHKIFEW---- 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 215 CVNMDGQMANMILDDGGDILT-----HWVYKYY-----PN 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 118 --HGGYVNLILDDGGDALTLLCVLGPKAEDPSILNPNQNEEBEALYAVMKKYLAEPKG 174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 244 VFKKIR---GIVSESVTVGHRLYOLSKAGKLCVPMANVNDSTVKQFPDNLCCRESILD 299
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 FYSAIRAAIGVSEETTVGHRLYOLSKAGKLCVPMANVNDSTVKQFPDNLCCRESILD 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 300 GKRTTDMVFGKQVAVCGYGEVKGCCALAKALGAIIVYTEIDIPICALQACMDGFRVVK 359
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 225 AIRRGTDVLSGKVAVCGYGVGKGSASLQSGARVIVTEVDPICALQAAMEGYEYQT 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 360 LNEVIRQDVVITCTGNKRVVTRHLDKMKNSCIYCNMGHSTELDVTSLRTPELTWERY 419
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 295 LNDVADKADIPTATGNKQVITVDMDKMKNNAIYCNIGHFSEIOIAGLR--NFKWDEI 352
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 420 RSQVDHVIMPDGKRVVLLAGRLNLNLSCT-VPTFVLSTATTQALALIELYNAPGRYK 478
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 353 KQVHHVEFPDQKLIIVLSEGRVNLGNATGHSFVMSASFTNQTIAQTELM-TNKAYE 411
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 479 QDVYLLPKMKDEVASLHLPSPDHALTELTDQAKYLGINKGPFKNYRY 530
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 412 NGVYLLPKHLDEKVALHLHGKLGARLTKLKSDQSDYVSIPIGPYKPHY 463
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:15:48 ; Search time 271.337 Seconds
(without alignments)
1806.825 Million cell updates/sec

Title: US-10-683-610-1
Perfect score: 2781
Sequence: 1 MSMPDAMPLEGVGSELKQAK.....QAKTLGKNGKPFKNRYRY 530

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2781	100.0	530	2	Q96PK4 HUMAN
2	2781	100.0	530	2	Q80SW1 MOUSE
3	2781	100.0	530	2	Q2TAJ6 HUMAN
4	2781	100.0	607	2	Q502W8 HUMAN
5	2781	100.0	623	2	Q6P171 HUMAN
6	2627	94.5	500	1	SAHH2 HUMAN
7	2579	92.7	505	2	Q2NKK8 HUMAN
8	2548	91.6	484	2	Q9UG84 HUMAN
9	2542	91.4	483	2	Q5VSM0 HUMAN
10	2469	88.8	540	2	Q5F3Q3 CHICK
11	2465	88.7	512	2	Q7T2B5 BRARE
12	2465	88.7	554	2	Q49S42 BRARE
13	2459	88.4	520	2	Q6E1P1 XENLA
14	2456	88.3	611	1	SAHH3 HUMAN
15	2454	88.2	613	1	Q68FL4 MOUSE
16	2446.5	88.0	588	2	Q5BL43 XENTR
17	2440	87.7	500	2	Q49S41 BRARE
18	2439	87.7	508	2	Q8B1H1 MOUSE
19	2438.5	87.5	588	2	Q68EX1 XENLA
20	2433	87.5	491	2	Q4RXQ1 TETNG
21	2430	87.4	508	2	Q5R889 PONPY
22	2427	87.3	530	2	Q6ZNS6 HUMAN
23	2410	86.7	591	2	Q6PC06 BRARE
24	2408	86.6	583	2	Q6AZU3 XENLA
25	2313.5	83.2	583	2	Q4RTV3 TETNG
26	2278	81.9	478	2	Q80T09 MOUSE
27	2182	78.5	541	2	Q4RHJ7 TETNG
28	1970	70.8	521	2	Q9VZX9 DROSOPHILA
29	1966	70.7	521	2	Q6NR07 DROSOPHILA
30	1826.5	65.7	492	1	SAHH2 DROSOPHILA
31	1819.5	65.4	504	2	Q7KSG0 DROSOPHILA

ALIGNMENTS

```

RESULT 1
Q96PK4 HUMAN PRELIMINARY; PRT; 530 AA.
AC Q96PK4:
DT 01-DEC-2001, integrated into UniProtKB/TREMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-MAR-2006, entry version 25.
DE Adenosylhomocysteine lyase (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-
DE homocysteine hydrolase).
GN Name=AHCYL1; ORFNames=RP11-180N18.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21901265; PubMed=11904675; DOI=10.1007/s00251-001-0402-z;
RA Dekker J.W., Budhia S., Angel N.Z., Cooper B.O., Clark G.J.,
RA Hart D.N., Kato M.,
RT "Identification of an S-adenosylhomocysteine hydrolase-like transcript
RT induced during dendritic cell differentiation.";
RL Immunogenetics 53:993-1001 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP Martin S.;
RA Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
CC homocysteine + adenosine.
CC -1- COPFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine lyase family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivative License
CC
EMBL: AF315687; AL26869.1; -; mRNA.
EMBL: AL772411; CAH70965.1; -; Genomic DNA.
HSSP: P10760; 1B3R.
DR Ensembl: ENSG00000168710; Homo sapiens.
DR GO: GO:0004013; F:adenosylhomocysteine lyase activity; IEA.
DR GO: GO:0016787; F:hydrolyase activity; IEA.
DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro: IPR013321; Ad_hcy_hydrolase.
DR InterPro: IPR013321; Ad_hcy_hydrolase.
DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF00670; AdoHcyase; NAD; 1.
DR TIGRFAMs: TIGR00936; ahcy; 1.
DR PROSITE: PS00738; ADOHCYASE_1; 1.
DR PROSITE: PS00739; ADOHCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
SQ SEQUENCE 530 AA; 58951 MW; 9740D3361A245D04 CRC64;

```

```

Query Match      100.0%; Score 2781; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDMPRLPGVGEELKQAKIEDAKESFMATVTKAPKKQIQFADDMOEFTKPTKTR 60
DB 1 MSMPDMPRLPGVGEELKQAKIEDAKESFMATVTKAPKKQIQFADDMOEFTKPTKTR 60
QY 61 RLSRSISOSTSDSYSSAASYTDSDEVS PREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
DB 61 RLSRSISOSTSDSYSSAASYTDSDEVS PREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
QY 121 ETABODMSALLSRKQAGSKPLAKAKIVGCTHTTQTVLIEFTLCALGAQCRWSACN1Y 180
DB 121 ETABODMSALLSRKQAGSKPLAKAKIVGCTHTTQTVLIEFTLCALGAQCRWSACN1Y 180
QY 181 STONEVAALALAEAGVAVFPAKGESEDDFMWCIDRCVNMGMQAMNLLDDGGDLTHVYVK 240
DB 181 STONEVAALALAEAGVAVFPAKGESEDDFMWCIDRCVNMGMQAMNLLDDGGDLTHVYVK 240
QY 241 YENVEFKIRIGIVEESVTGVHRLYQLSKAGKLCVPAWNVNDSVTKQKFDNLCCRESILDG 300
DB 241 YENVEFKIRIGIVEESVTGVHRLYQLSKAGKLCVPAWNVNDSVTKQKFDNLCCRESILDG 300
QY 301 LKRTDVMGSGQVYVCGYGEVKGCCALKALGAVITTEIDPICALQACMDGFRVVL 360
DB 301 LKRTDVMGSGQVYVCGYGEVKGCCALKALGAVITTEIDPICALQACMDGFRVVL 360
QY 361 NEVIRQVDVITCTGNKAVVTRHRLMRKNSCVCNMGSNFEIDVTSRLTELTMYERV 420
DB 361 NEVIRQVDVITCTGNKAVVTRHRLMRKNSCVCNMGSNFEIDVTSRLTELTMYERV 420
QY 421 SQVDHVIWPDGKRVLLAEGRLNLSCTVPTFVLSITATQALALIELYNAPGRRYKOD 480
DB 421 SQVDHVIWPDGKRVLLAEGRLNLSCTVPTFVLSITATQALALIELYNAPGRRYKOD 480
QY 481 VVLPKMDYVVASLHLPSFDAHLTELTDQAKYLGANNGPKPKYRY 530
DB 481 VVLPKMDYVVASLHLPSFDAHLTELTDQAKYLGANNGPKPKYRY 530

RESULT 2
Q80SM1_MOUSE PRELIMINARY; PRT; 530 AA.
AC Q80SM1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-MAR-2006, entry version 26.
DE S-adenosylhomocysteine hydrolase-like 1 (IP3R binding protein released with inositol 1,4,5-trisphosphate) (S-adenosylhomocysteine hydrolase-like protein).
GN Name=Ancyl1; Synonyma=Ibdl1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Mus.
OC NCBI_TaxID=10090;
[1]
NUCLEOTIDE SEQUENCE.
RC STRAIN-Czech II; Tissue=Mammary tumor metastasized to lung.
RC MMTV-LTR/Mutl model. Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schaller G.D., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hylk S.W., Villalón D.K., Mueny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

```

```

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN (2)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN-Czech II; Tissue=Mammary tumor metastasized to lung.
RC MMTV-LTR/Mutl model. Expression driven by an MMTV-LTR enhancer.;
RG NIH MGC Project;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN (3)
RP NUCLEOTIDE SEQUENCE.
RC Tissue=Cerebellum;
RX MEDLINE=22526701; PubMed=12525476; DOI=10.1074/jbc.M210119200;
RA Ando H., Mizutani A., Matsui T., Mikoshida K.;
RT "IRBIT, a novel inositol 1,4,5-trisphosphate (IP3) receptor-binding
RT protein, is released from the IP3 receptor upon IP3 binding to the
RT receptor."
RL J. Biol. Chem. 278:10602-10612(2003).
RN (4)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21901265; PubMed=11904675; DOI=10.1007/s00251-001-0402-2;
RA Dekker J.W., Budhia S., Angel N.Z., Cooper B.J., Clark G.J.,
RA Hart D.N., Kato M.;
RT "Identification of an S-adenosylhomocysteine hydrolase-like transcript
RT induced during dendritic cell differentiation."
RL Immunogenetics 53:993-1001(2002).
CC -1- MICELANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
CC homocysteine + adenosine.
CC -1- COFACTOR: NAD (by similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
DR EMBL: BC018218; AAH18218.2; -; mRNA.
DR EMBL: AB092504; BAC65166.1; -; mRNA.
DR EMBL: BK000547; DAA00059.1; -; mRNA.
DR HSSP: P10760; 1B3R.
DR Ensemble; ENSMUSG0000027893; Mus musculus.
DR MGI: MGI:2385184; Ancy11.
DR GO: GO:0004013; F:adenosylhomocysteine activity; RCA.
DR GO: GO:0016787; F:hydrolase activity; RCA.
DR GO: GO:0006730; P:one-carbon compound metabolism; RCA.
DR InterPro: IPR000043; Ad_hcy_hydrolase.
DR InterPro: IPR013321; Ad_hcn_hlx_hlx.
DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF0670; AdoHcyase_NAD; 1.
DR TIGRFAMs: TIGR00936; ahcy; 1.
DR PROSITE: PS00738; ADOHCYASE_1; 1.
DR PROSITE: PS00739; ADOHCYASE_2; 1.
DR Hydrolase; NAD; One-carbon metabolism.
SQ SEQUENCE 530 AA; 58951 MW; 974D23361A245D04 CRC64;

```

```

Query Match      100.0%; Score 2781; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 6.3e-208;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDMPRLPGVGEELKQAKIEDAKESFMATVTKAPKKQIQFADDMOEFTKPTKTR 60
DB 1 MSMPDMPRLPGVGEELKQAKIEDAKESFMATVTKAPKKQIQFADDMOEFTKPTKTR 60
QY 61 RLSRSISOSTSDSYSSAASYTDSDEVS PREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
DB 61 RLSRSISOSTSDSYSSAASYTDSDEVS PREKQOTNSKSSNFCVKNIKQAEFGRRRI 120

```

Db 61 RSLRSISQSSTDSYSSAASYTDSSEDESPREKQNTSKSSNFCVNIKAQERGREI 120
Qy 121 EIAQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCALGAOCRMSACNIY 180
Db 121 EIAQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCALGAOCRMSACNIY 180
Qy 181 STOREVAAALAEAGVAFAMKGESEDFWMCIDRCVNMNDGQAMNIIIDDGDLTHWYKK 240
Db 181 STOREVAAALAEAGVAFAMKGESEDFWMCIDRCVNMNDGQAMNIIIDDGDLTHWYKK 240
Qy 241 YPNVFKKIRGIVESVTGVRHLVYOLSKAGKLCVPMANVNDVTKQFNDLYCCRESIIDG 300
Db 241 YPNVFKKIRGIVESVTGVRHLVYOLSKAGKLCVPMANVNDVTKQFNDLYCCRESIIDG 300
Qy 301 LKRTTDMFGKQVYVCGYGVGKCCCAALKALGAIYITTEIDPICALQACMDGFRVYKL 360
Db 301 LKRTTDMFGKQVYVCGYGVGKCCCAALKALGAIYITTEIDPICALQACMDGFRVYKL 360
Qy 361 NEVIRQDVVITTCGNKNVVTREHLDKMKNSCIYCMNGHSTETIDVSLRTPELTWERVR 420
Db 361 NEVIRQDVVITTCGNKNVVTREHLDKMKNSCIYCMNGHSTETIDVSLRTPELTWERVR 420
Qy 421 SOVDHVIMPDGKRVVLLAEGRLNLSCTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
Db 421 SOVDHVIMPDGKRVVLLAEGRLNLSCTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
Qy 481 VYLLPKKMDDEVASLHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530
Db 481 VYLLPKKMDDEVASLHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530

RESULT 3
Q2TAJ6_HUMAN PRELIMINARY; PRT; 599 AA.
ID Q2TAJ6_HUMAN
AC Q2TAJ6
DT 24-JUN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JUN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE AHCYL1 protein (Fragment).
GN Name=AHCYL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN NCBI [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Uscin T.B., Toshlyuk S., Carrinci P., Prange C.,
RA Raha S.S., Loquelelano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Holton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RC NIM MGC Project;

RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
CC homocysteine + adenosine.
CC -I- COFACTOR: NAD (by similarity).
CC -I- PATHWAY: Activated methyl cycle.
CC -I- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
CC EMBL: BC110896; AAI10897.1; -, mRNA.
CC Hydroxylase; NAD; One-carbon metabolism.
FT NON TER 1
SQ SEQUENCE 599 AA; 65700 MW; CBSBAEB1950CEAAB CRC64;
Query Match 100.0%; Score 2781; DB 2; Length 599;
Best Local Similarity 100.0%; Pred. No. 7, se-208;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSMDAMPPLPGVGEELKQAKIEDAEKYSFMAVYTKAPKQIOPADMOEFTKPTKGR 60
Db 70 MSMDAMPPLPGVGEELKQAKIEDAEKYSFMAVYTKAPKQIOPADMOEFTKPTKGR 129
Qy 61 RSLRSISQSSTDSYSSAASYTDSSEDESPREKQNTSKSSNFCVNIKAQERGREI 120
Db 130 RSLRSISQSSTDSYSSAASYTDSSEDESPREKQNTSKSSNFCVNIKAQERGREI 189
Qy 121 EIAQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCALGAOCRMSACNIY 180
Db 190 EIAQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCALGAOCRMSACNIY 249
Qy 181 STOREVAAALAEAGVAFAMKGESEDFWMCIDRCVNMNDGQAMNIIIDDGDLTHWYKK 240
Db 250 STOREVAAALAEAGVAFAMKGESEDFWMCIDRCVNMNDGQAMNIIIDDGDLTHWYKK 309
Qy 241 YPNVFKKIRGIVESVTGVRHLVYOLSKAGKLCVPMANVNDVTKQFNDLYCCRESIIDG 300
Db 310 YPNVFKKIRGIVESVTGVRHLVYOLSKAGKLCVPMANVNDVTKQFNDLYCCRESIIDG 369
Qy 301 LKRTTDMFGKQVYVCGYGVGKCCCAALKALGAIYITTEIDPICALQACMDGFRVYKL 360
Db 370 LKRTTDMFGKQVYVCGYGVGKCCCAALKALGAIYITTEIDPICALQACMDGFRVYKL 429
Qy 361 NEVIRQDVVITTCGNKNVVTREHLDKMKNSCIYCMNGHSTETIDVSLRTPELTWERVR 420
Db 430 NEVIRQDVVITTCGNKNVVTREHLDKMKNSCIYCMNGHSTETIDVSLRTPELTWERVR 489
Qy 421 SOVDHVIMPDGKRVVLLAEGRLNLSCTVPTFVLSTATTQALALIELYNAPBGRYKOD 480
Db 490 SOVDHVIMPDGKRVVLLAEGRLNLSCTVPTFVLSTATTQALALIELYNAPBGRYKOD 549
Qy 481 VYLLPKKMDDEVASLHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 530
Db 550 VYLLPKKMDDEVASLHLPSPFAHLTELTDQAKYLGLNKGPFKNYRY 599

RESULT 4
Q502W8_HUMAN PRELIMINARY; PRT; 607 AA.
ID Q502W8_HUMAN
AC Q502W8;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN NCBI [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marnusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 CC NUCLEOTIDE SEQUENCE.
 CC TISSUE=Peripheral Nervous System;
 CC NIH MC Project;
 CC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 CC EMBL: BC095476; AAH95476.1; -; mRNA.
 CC Ensembl: ENSG00000168710; Homo sapiens.
 DR GO: GO:0004013; F:adenosylhomocysteine activity; IEA.
 DR GO: GO:0016787; F:hydrolyase activity; IEA.
 DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro: IPR000043; Ad_hcy_hydrolyase.
 DR InterPro: IPR013321; Arc_rhn_hlx_hlx.
 DR InterPro: IPR01128; Cytochrome P450.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolyase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase; 1.
 DR TIGRFAMs: TIGR00936; ahcy; 1.
 DR PROSITE: PS00738; ADHCYASE_1; 1.
 DR PROSITE: PS00739; ADHCYASE_2; UNKNOWN_1.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Hydrolyase; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON_TER 1
 FT SEQUENCE 607 AA; 66683 MW; 349412833E2D5911 CRC64;
 SQ
 Query Match 100.0%; Score 2781; DB 2; Length 607;
 Best Local Similarity 100.0%; Pred. No. 7.6e-208;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 241 YPNVFKIRIGVEESVTGVRHLVYLSKAGKLCVPAANNVDSVTKQKPNLYCCRESIIDG 300
 DB 318 YPNVFKIRIGVEESVTGVRHLVYLSKAGKLCVPAANNVDSVTKQKPNLYCCRESIIDG 377
 QY 301 LKRTTDMFGSKQVVGCGYGVGGCCALKALGIVITSIDPICALQACMDGRRVYL 360
 DB 378 LKRTTDMFGSKQVVGCGYGVGGCCALKALGIVITSIDPICALQACMDGRRVYL 437
 QY 361 NEVIROYDVVTTCGNKVVTRHLDKMKSCIVCNMGHSTEDIVTSLRTPELTWBRV 420
 DB 438 NEVIROYDVVTTCGNKVVTRHLDKMKSCIVCNMGHSTEDIVTSLRTPELTWBRV 497
 QY 421 SQDVHVWPGKRVYLAEGLLNLSCSTVTPVLSTATTQALALIELNAPBGRYKOD 480
 DB 498 SQDVHVWPGKRVYLAEGLLNLSCSTVTPVLSTATTQALALIELNAPBGRYKOD 557
 QY 481 VYLLPKKMDVYASLHLPSFPAHLTELDDPAKYLGLKNGKPPKPNYRY 530
 DB 558 VYLLPKKMDVYASLHLPSFPAHLTELDDPAKYLGLKNGKPPKPNYRY 607

RESULT 5
 06P171_HUMAN PRELIMINARY; PRT; 623 AA.
 ID 06P171_HUMAN
 AC 06P171
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 13.
 DE 07-FEB-2006, entry version 13.
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RP TISSUE=Eye.
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marnusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 CC NUCLEOTIDE SEQUENCE.
 CC TISSUE=Eye;
 CC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 CC EMBL: BC065254; AAH65254.1; -; mRNA.

DR HSPB; P10760; 1B3R.
 DR Ensembl; ENSG00000168710; Homo sapiens.
 DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad_hcy hydrolyase.
 DR InterPro; IPR013321; Arc_rbn_hlx_hlx.
 DR InterPro; IPR01128; Cytochrome_P450.
 DR PANTHER; PTHR11784; Ad_hcy_hydrolyase; 1.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF0670; AdoHcyase_NAD; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Hydrolyase; Hydrolyase; NAD; One-carbon metabolism.
 FT NON_TER 1
 FT SEQUENCE 623 AA; 68648 MW; B0A40ED58BAF3F23 CRC64;
 Query Match 100.0%; Score 2781; DB 2; Length 623;
 Best Local Similarity 100.0%; Pred. No. 7.9e-208;
 Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MSMPDAMP; PGVGBELKQAKEDIEDEKTSFMAVTAKAPKOIQFADDMOEFTKPTKGR 60
 Db 94 MSMPDAMP; PGVGBELKQAKEDIEDEKTSFMAVTAKAPKOIQFADDMOEFTKPTKGR 153
 Oy 61 RLSRSISQSSSTDSYSSAASYTSSDSDSESPREKQNTSKSSNFCVKNIKQAEFRREI 120
 Db 154 RLSRSISQSSSTDSYSSAASYTSSDSDSESPREKQNTSKSSNFCVKNIKQAEFRREI 213
 Oy 121 EIAEDMSALISLRKAGGKPLAKAVCGTHITAOAVLIEITCALGAGCGRMAGNITY 180
 Db 214 EIAEDMSALISLRKAGGKPLAKAVCGTHITAOAVLIEITCALGAGCGRMAGNITY 273
 Oy 181 STONEVAALAEAGAVAFAMKGESEDDFMWCIDRCVNDGMOAMNILDGGLTFHWYKK 240
 Db 274 STONEVAALAEAGAVAFAMKGESEDDFMWCIDRCVNDGMOAMNILDGGLTFHWYKK 333
 Oy 241 YPNVFKIRGIVESVTGVHRLYQLSKAGKLCVPMANVNDSTYKQFNNLYCCRESILDG 300
 Db 334 YPNVFKIRGIVESVTGVHRLYQLSKAGKLCVPMANVNDSTYKQFNNLYCCRESILDG 393
 Oy 301 LKRTDWFEGKQVNVCGYGVGKCCALAKALGIYITTEIDPICALQACMDGFRVVKL 360
 Db 394 LKRTDWFEGKQVNVCGYGVGKCCALAKALGIYITTEIDPICALQACMDGFRVVKL 453
 Oy 361 NEVTRQDVVITTCGNKQVNVREHLDKMKNSCIVCMGHSNTEIDVTSILRTPELTWEVR 420
 Db 454 NEVTRQDVVITTCGNKQVNVREHLDKMKNSCIVCMGHSNTEIDVTSILRTPELTWEVR 513
 Oy 421 SQVDHVIMPDGKRVVLAEGRLNLSCSTVPFVLSTATTQALLIELYNAPGGRYKOD 480
 Db 514 SQVDHVIMPDGKRVVLAEGRLNLSCSTVPFVLSTATTQALLIELYNAPGGRYKOD 573
 Oy 481 VYLLPKKMDDEVASLHLPSPDAHTELTDQAKTIGLNKGPFKNYRY 530
 Db 574 VYLLPKKMDDEVASLHLPSPDAHTELTDQAKTIGLNKGPFKNYRY 623
 RESULT 6
 SAH2 HUMAN STANDARD; PRT; 500 AA.
 ID SAH2 HUMAN STANDARD; PRT; 500 AA.
 AC 043865;
 DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1998, sequence version 1.
 DT 07-MAR-2006, entry version 44.
 DE Putative adenosylhomocysteinease 2 (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolyase) (AdoHcyase).
 GN Name=AHCYL1; Synonyms=XPVXONA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

CC Homo.
 OK NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [mRNA].
 RC TISSUE=SKIN.
 RA Volpe J.P.G., McDowell M., Joates R.F., Afzal V., Sadinaki W.,
 RA Trank B.J., Legerski R., Cleaver J.E.,
 RT "Complementation of chromosomal instability in the xeroderma
 RT pigmentosa variant by a gene on human chromosome 1 with homology to
 RT S-adenosyl homocysteine hydrolyase."
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Colon, and Placenta.
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshynski S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalski U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-homocysteine + adenosine.
 CC -1- CORFACTOR: Binds 1 NAD per subunit (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DR EMBL; U82761; AAC01960.1; -; mRNA.
 DR EMBL; BC007576; AAH07576.1; -; mRNA.
 DR EMBL; BC010681; AAH10681.1; -; mRNA.
 DR EMBL; BC016942; AAH16942.1; -; mRNA.
 DR HSPB; P10760; 1B3R.
 DR Ensembl; ENSG00000168710; Homo sapiens.
 DR HGNC; HGNC:344; AHCYL1.
 DR MIM; 607826; Gene.
 DR InterPro; IPR000043; Ad_hcy hydrolyase.
 DR InterPro; IPR013321; Arc_rbn_hlx_hlx.
 DR PANTHER; PTHR11784; Ad_hcy_hydrolyase; 1.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF0670; AdoHcyase_NAD; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 DR Hydrolyase; NAD; One-carbon metabolism.
 KW CHAIN 1 500
 FT REGION 251 418
 FT BINDING 125 125 NAD binding (By similarity).
 FT BINDING 199 199 Substrate (By similarity).
 FT BINDING 224 224 Substrate (By similarity).
 FT BINDING 254 254 Substrate (By similarity).
 FT BINDING 258 258 Substrate (By similarity).
 FT SEQUENCE 500 AA; 55628 MW; FDEABFC70044B9DA CRC64;
 Query Match 94.5%; Score 2627; DB 1; Length 500;
 Best Local Similarity 100.0%; Pred. No. 6e-196;

Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 MATVTAPKKOIOFADDMOEFTKPTKTRSRISRSISQSTDSYSSAASYTDSDEVS 90
 1 MATVTAPKKOIOFADDMOEFTKPTKTRSRISRSISQSTDSYSSAASYTDSDEVS 60

QY 91 PREKOQTNKSGSSNFCVKNI KOAEFGREIEIAEQMSALISLRKRAQGEKPLAGAKIVG 150
 61 PREKOQTNKSGSSNFCVKNI KOAEFGREIEIAEQMSALISLRKRAQGEKPLAGAKIVG 120

QY 151 CHHTAQTAVLTETLALCAQCRWSACNISTONEVAAALAEAGVAVPAMKGSSEDDPMW 210
 121 CHHTAQTAVLTETLALCAQCRWSACNISTONEVAAALAEAGVAVPAMKGSSEDDPMW 180

QY 211 CIDRCVNMGMQAMNMLDDGGDLTHWVYKKYPNVFKIRIGIVESVTGVHRLYQLSKAK 270
 181 CIDRCVNMGMQAMNMLDDGGDLTHWVYKKYPNVFKIRIGIVESVTGVHRLYQLSKAK 240

QY 271 LCVPMANVNDSTVKQKFDNLVCCRESILDLGKRTTDMVFGKOVVVCYGEVKGCCAL 330
 241 LCVPMANVNDSTVKQKFDNLVCCRESILDLGKRTTDMVFGKOVVVCYGEVKGCCAL 300

QY 331 KALGAVVYTEIDPICALQACMDGFRVVKLNEVIRQVDVITCTGNKVVTREHLDPMK 390
 301 KALGAVVYTEIDPICALQACMDGFRVVKLNEVIRQVDVITCTGNKVVTREHLDPMK 360

QY 391 SCIVCMGHSNTEIDVTSLRTPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSGSTV 450
 361 SCIVCMGHSNTEIDVTSLRTPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSGSTV 420

QY 451 PTFVLSITATTOALALIELYNAPBGRYKQDVYLLPKKMDVYASLHLPSPDAHTELTD 510
 421 PTFVLSITATTOALALIELYNAPBGRYKQDVYLLPKKMDVYASLHLPSPDAHTELTD 480

QY 511 QAKYGLNKGPKPNYYR 530
 481 QAKYGLNKGPKPNYYR 500

Db

RESULT 7
 Q2NKM8_HUMAN PRELIMINARY; PRT; 505 AA.
 AC Q2NKM8;
 DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DE 07-FEB-2006, entry version 1.
 DE AHCVL1 protein (Fragment).
 GN Name-AHCVL1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP TISSUE=PCR rescued clones;
 RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Hsieh F.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loughlano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=PCR rescued clones;
 RG NIH MGC Project;
 RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 DR EMBL; BC11563; A011564.1; -; mRNA.
 CC NON TER
 FT SEQUENCE 505 AA; 56469 MW; 0231B614A22D5662 CRC64;
 SQ

Query Match 92.7%; Score 2579; DB 2; Length 505;
 Best Local Similarity 99.8%; Pred. No. 3.4e-192;
 Matches 490; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 40 KOIOFADDMOEFTKPTKTRSRISRSISQSTDSYSSAASYTDSDEVS PREKOQTN 99
 :
 Db 15 QOIQFADDMOEFTKPTKTRSRISRSISQSTDSYSSAASYTDSDEVS PREKOQTN 74

QY 100 KSSNFCVKNI KOAEFGREIEIAEQMSALISLRKRAQGEKPLAGAKIVGCHTITAQTA 159
 75 KSSNFCVKNI KOAEFGREIEIAEQMSALISLRKRAQGEKPLAGAKIVGCHTITAQTA 134

QY 160 VLEITLALCAQCRWSACNISTONEVAAALAEAGVAVPAMKGSSEDDPMW CIDRCVNM 219
 135 VLEITLALCAQCRWSACNISTONEVAAALAEAGVAVPAMKGSSEDDPMW CIDRCVNM 194

QY 220 GWOANMLDDGGDLTHWVYKKYPNVFKIRIGIVESVTGVHRLYQLSKAKLCPMANNV 279
 195 GWOANMLDDGGDLTHWVYKKYPNVFKIRIGIVESVTGVHRLYQLSKAKLCPMANNV 254

QY 280 DSVTKQKFDNLVCCRESILDLGKRTTDMVFGKOVVVCYGEVKGCCALALGAIYV 339
 255 DSVTKQKFDNLVCCRESILDLGKRTTDMVFGKOVVVCYGEVKGCCALALGAIYV 314

QY 340 TELDPICALQACMDGFRVVKLNEVIRQVDVITCTGNKVVTREHLDPMKNSCIVCMG 399
 315 TELDPICALQACMDGFRVVKLNEVIRQVDVITCTGNKVVTREHLDPMKNSCIVCMG 374

QY 400 SNTIEDVTSLRTPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSGSTVPTFVLSITA 459
 375 SNTIEDVTSLRTPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSGSTVPTFVLSITA 434

QY 460 TFOALALIELYNAPBGRYKQDVYLLPKKMDVYASLHLPSPDAHTELTDQAKYGLNK 519
 435 TFOALALIELYNAPBGRYKQDVYLLPKKMDVYASLHLPSPDAHTELTDQAKYGLNK 494

Db

QY 520 NGPFKPNYYR 530
 495 NGPFKPNYYR 505

Db

RESULT 8
 Q9UG84_HUMAN PRELIMINARY; PRT; 484 AA.
 AC Q9UG84;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 2.
 DE 07-FEB-2006, entry version 23.
 DE Adenosylhomocysteinease (EC 3.3.1.1) (AdoHCyase) (S-adenosyl-L-homocysteine hydrolase) (Fragment).
 GN Name-DKRP564A1523;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;

RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RG The German cDNA Consortium;
 RA Mambuti R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fodor G., Han M., Wiemann S.;
 CC Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL, AL049954, CAB43223.2; -, mRNA.
 CC PIR, T08681, T08681.
 CC Ensembl: ENSG00000168710; Homo sapiens.
 CC GO: GO:0004013; F:adenosylhomocysteine activity; IEA.
 CC GO: GO:0016787; F:hydrolyase activity; IEA.
 CC GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 CC InterPro: IPR000043; Ad_hcy_hydrolyase.
 CC PANTHER: PTHR11784; Ad_hcy_hydrolyase; 1.
 CC Pfam: PF05221; AdoHcyase; 1.
 CC Pfam: PF00670; AdoHcyase_NAD; 1.
 CC TIGRfam: TIGR00936; ahcy; 1.
 CC PROSITE, PS00738; ADOHCYASE_1; 1.
 CC PROSITE, PS00739; ADOHCYASE_2; 1.
 CC Hydrolyase; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON TER 1
 SQ SEQUENCE 484 AA; 5369 MW; 8A55FE646B7E1D CRC64;
 Query Match 91.6%; Score 2548; DB 2; Length 484;
 Best Local Similarity 100.0%; Pred. No. 8.4e-190;
 Matches 484; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9
 OS=USMO_HUMAN
 ID 05VSMO_HUMAN PRELIMINARY; PRT; 483 AA.
 AC 05VSMO;
 DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Adenosylhomocysteinease (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-
 DE homocysteine hydrolase).
 GN Name=AHCYL; ORFNames=RP11-180N18.1-002;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN NUCLEOTIDE SEQUENCE.
 RP Martin S.;
 RA Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial License
 CC -----
 CC EMBL, AL772411; CAH70966.1; -, Genomic DNA.
 CC Ensembl: ENSG00000168710; Homo sapiens.
 CC GO: GO:0004013; F:adenosylhomocysteine activity; IEA.
 CC GO: GO:0016787; F:hydrolyase activity; IEA.
 CC GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 CC InterPro: IPR000043; Ad_hcy_hydrolyase.
 CC PANTHER: PTHR11784; Ad_hcy_hydrolyase; 1.
 CC Pfam: PF05221; AdoHcyase; 1.
 CC Pfam: PF00670; AdoHcyase_NAD; 1.
 CC TIGRfam: TIGR00936; ahcy; 1.
 CC PROSITE, PS00738; ADOHCYASE_1; 1.
 CC PROSITE, PS00739; ADOHCYASE_2; 1.
 CC Hydrolyase; NAD; One-carbon metabolism.
 SQ SEQUENCE 483 AA; 53753 MW; 18DFC7E74697E1D4 CRC64;
 Query Match 91.4%; Score 2542; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 2.4e-189;
 Matches 483; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

DB 361 SARTBELTWERRSQVDHVIWPDGKRVLLAEGRLNLSCSTVPTFVLSTATTQALALI 420
QY 468 ELYNAPBGRYKODVYLLPKKMDYVVASLHLPFDALHTELTDQAKYLGLNKGPKPNV 527
DB 421 ELYNAPBGRYKODVYLLPKKMDYVVASLHLPFDALHTELTDQAKYLGLNKGPKPNV 480
QY 528 YRY 530
DB 481 YRY 483

RESULT 10
05F303 CHICK PRELIMINARY; PRT; 540 AA.
ID 05F303_
AC 05F303_
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein.
GN ORFNames=RCJM04.10b17;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CB; TISSUE=Bursa;
RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
RA Fiedler P., Kutter S., Blagoderatski A., Kostovska D., Kotter M.,
RA Plachy J., Carninci P., Hayashizaki Y., Buettstedt J.M.,
RA "Full-length cDNAs from chicken bursal lymphocytes to facilitate
RT gene function analysis."
RL Genome Biol. 6:R6-R6(2005).
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC distributed under the Creative Commons Attribution-NonDerivs license
CC -----
EMBL: AJ851597; CAH5231.1; -, mRNA.
DR GO; GO:0004013; P:adenosylhomocysteinease activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR000043; Ad_hcy_hydrolyase.
DR InterPro; IPR013321; Arc_rhn_hlx_hlx.
DR PANTHER; PTHR11784; Ad_hcy_hydrolyase; 1.
DR Pfam; PF005221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
DR KMW Hypothetical protein.
SQ SEQUENCE 540 AA; 59231 MW; 668479BFA2368F92 CRC64;

Query Match 88.8%; Score 2469; DB 2; Length 540;
Best Local Similarity 95.7%; Pred. No. 1,4e-183;
Matches 473; Conservative 8; Mismatches 9; Indels 4; Gaps 1;

```

```

QY 241 YENVEFKIRGIYESVTGVRHLYQLSKAGKLCVPAMNVDSYTKQFDMLYCCRESILDG 300
DB 237 YENIFPKIRGIYESVTGVRHLYQLSKAGKLCVPAMNVDSYTKQFDMLYCCRESILDG 296
QY 301 LKRTDVMFGKQVAVCCGVEGKCCCAALKALGAIYVTEIDPICALQACMDGFRVVKL 360
DB 297 LKRTDVMFGKQVAVCCGVEGKCCCAALKALGAIYVTEIDPICALQACMDGFRVVKL 356
QY 361 NEVIRQVDVITCTGNKRVVTFREHIDRMKNSCIYCMGHSNTEIDVTSIRTELTWERVR 420
DB 357 SEVIRQVDVITCTGNKRVVTFREHIDRMKNSCIYCMGHSNTEIDVTSIRTELTWERVR 416
QY 421 SQVDHVIWPDGKRVLLAEGRLNLSCSTVPTFVLSTATTQALALI ELYNAPBGRYKOD 480
DB 417 SQVDHVIWPDGKRVLLAEGRLNLSCSTVPTFVLSTATTQALALI ELYNAPBGRYKOD 476
QY 481 VYLLPKKMDYVVAS 494
DB 477 VYLLPKKMDGSRPS 490

RESULT 11
07T2B5 BRARE PRELIMINARY; PRT; 512 AA.
ID 07T2B5_BRARE
AC 07T2B5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE S-adenosylhomocysteine hydrolase-like 1.
GN Name=ahcy11; reio (Zebrafish) (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Strausberg R.;
RA Submitter (Jul-2003) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC distributed under the Creative Commons Attribution-NonDerivs license
CC -----
EMBL: BC054614; AAH54614.1; -, mRNA.
DR HSSP; P10760; 1B3R.
DR ZFIN; ZDB-GENE-021206-7; ahcy11.
DR GO; GO:0004013; P:adenosylhomocysteinease activity; IEA.
DR GO; GO:0016787; P:hydrolase activity; IEA.

```

DR GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro: IPR000043; Ad_hcy_hydrolase.
DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF00670; AdoHcyase_NAD; 1.
DR TIGRfams: TIGR00936; ahcy; 1.
DR PROSITE: PS00738; AdoHcyase_1; 1.
DR PROSITE: PS00739; AdoHcyase_2; 1.
KW Hydrolase.
SQ SEQUENCE 512 AA; 56776 MW; 3E0A09DFF086683 CRC64;

Query Match 88.7%; Score 2466; DB 2; Length 512;
Best Local Similarity 92.1%; Pred. No. 2,3e-183;
Matches 464; Conservative 22; Mismatches 16; Indels 2; Gaps 1;

QY 29 SFMATVTPAKPKQIOFA--DMQERTKPTKGRSLSRSSISQSTDSYSSAASYTSSD 86
DB 9 AFTAVPTKRSVKIOPANOEDKQEFKPTKGRSLSRSSISQSTDSYSSAASYTSSD 68
QY 87 DEVSPREKQNTSKSSNFCVNIKOAFGRREIADQMSALSLKRAQGEKPLAGA 146
DB 69 DETSPREKQNTSKSSNFCVNIKOAFGRREIADQMSALSLKRAQGEKPLAGA 128
QY 147 KIVGCTHTTAOTAVLIETLCALGACRMSACNIYSTONEVAALAEAGVAFAMKGESED 206
DB 129 KVAGCTHTTAOTAVLIETLVAGACRMTACNIYSTONEVAALAEAGVAFAMKGESED 188
QY 207 DFWMCIDRCVNMDSQANMILDDGDLTHWYKYPNVFKIRGIIESSVTGVHRLYQLS 266
DB 189 DFWMCIDRCVNMDSQANMILDDGDLTHWYKYPNVFKIRGIIESSVTGVHRLYQLS 248
QY 267 KAGLQCVPMNVNDSVTKOKFDNLVCCRESILDLKRTTDMFGKQVNVGCGVGKGC 326
DB 249 KAGLQCVPMNVNDSVTKOKFDNLVCCRESILDLKRTTDMFGKQVNVGCGVGKGC 308
QY 327 CAALKALGAIYITEIDPICALQACMDGFRVYKLVNEVROYDVITCTGNKNVVRHELD 386
DB 309 CSAALKALGAIYCVIEIDPICALQACMDGFRVYKLVNEVROYDVITCTGNKNVVRHELD 368
QY 387 RMKNSCIYCNMGHSNTEIDVTSRTPELTWERVSQVDHVIWPDGRVLLAEGRLLNL 446
DB 369 RMKNSCIYCNMGHSNTEIDVTSRTPELTWERVSQVDHVIWPDGRVLLAEGRLLNL 428
QY 447 CSTVPTFLSTATTQALALIELVNAPEGRYKQDVYLLPKMDEVVASHLPSPAHLTE 506
DB 429 CSTVPSFVLSITATTQALALIELVNAPEGRYKQDVYLLPKMDEVVASHLPSPAHLTE 488
QY 507 LTDDQAKYLGNKNGPFKNYRY 530
DB 489 LSDEQAKYMGINKNGPFKNYRY 512

RESULT 12
ID Q49S42_BRARE PRELIMINARY; PRT; 554 AA.
AC Q49S42_13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE S-adenosylhomocysteine hydrolase-like protein variant 1.
GN Name=ahcy11;
OS Breichdanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_Taxid=7955;
RN [1]
RA NUCLEOTIDE SEQUENCE.
RA Cooper B.J., Key B., Carter A., Angel N.Z., Jackson A., Hart D.N.J.,
RA Kato M.,
RT "Ectopic expression of adenosylhomocysteine hydrolase-like protein 1
RT (AHcy11) causes dorsalization of zebrafish embryos: Zebrafish AHcy11
RT cloning, gene structure and function.";

RU Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonCommercial License
CC -----
DR EMBL: AY611473; AAU02792.1; -; mRNA.
DR ZFIN: ZDB-GENE-021206-7; ahcy11.
DR GO:0004013; F:adenosylhomocysteinease activity; IEA.
DR GO:0016787; F:hydrolase activity; IEA.
DR GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro: IPR000043; Ad_hcy_hydrolase.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF00670; AdoHcyase_NAD; 1.
DR TIGRfams: TIGR00936; ahcy; 1.
DR PROSITE: PS00738; AdoHcyase_1; 1.
DR PROSITE: PS00739; AdoHcyase_2; UNKNOWN_1.
KW Hydrolase.
SQ SEQUENCE 554 AA; 61406 MW; 4E5F03E1D238A36 CRC64;

Query Match 88.7%; Score 2465.5; DB 2; Length 554;
Best Local Similarity 87.7%; Pred. No. 2,8e-183;
Matches 471; Conservative 24; Mismatches 19; Indels 23; Gaps 3;

QY 17 KOAKIED-AEKYS-----FMATVTAKPKQIOFA--DMQERTK 53
DB 18 KEFSESEVARKYAMATKSHDVNMVNGELSAFTAVPTKRSVKIOPANOEDKQEFK 77
QY 54 PPTKGRSLSRSSISQSTDSYSSAASYTSSDDEVSPREKQNTSKSSNFCVNIKO 113
DB 78 PPTKGRSLSRSSISQSTDSYSSAASYTSSDDEVSPREKQNTSKSSNFCVNIKO 137
QY 114 EFGREIEIAQDMSALSLKRAQGEKPLAGAKIVGCTHTTAOTAVLIETLCALGACR 173
DB 138 EFGREIEIAQDMSALSLKRAQGEKPLAGAKIVGCTHTTAOTAVLIETLVAGACR 197
QY 174 WSACNIYSTONEVAALAEAGVAFAMKGESEDFWMCIDRCVNMDSQANMILDDGDL 233
DB 198 WTACNIYSTONEVAALAEAGVAFAMKGESEDFWMCIDRCVNMDSQANMILDDGDL 257
QY 234 THWYKYPNVFKIRGIIESSVTGVHRLYQLSFAKGLCVPMNVNDSVTKOKFDNLVCC 293
DB 258 THWYKYPNVFKIRGIIESSVTGVHRLYQLSFAKGLCVPMNVNDSVTKOKFDNLVCC 317
QY 294 RESILDLKRTTDMFGKQVNVGCGVGKCCALKALGAIYITEIDPICALQACMD 353
DB 318 RESILDLKRTTDMFGKQVNVGCGVGKCCALKALGAIYITEIDPICALQACMD 377
QY 354 GFRVYKLVNEVROYDVITCTGNKNVVRHELDKNSCIYCNMGHSNTEIDVTSRTPE 413
DB 378 GFRVYKLVNEVROYDVITCTGNKNVVRHELDKNSCIYCNMGHSNTEIDVTSRTPE 437
QY 414 LTWERVSQVDHVIWPDGRVLLAEGRLLNLSCSTVPTFLSTATTQALALIELVNA 473
DB 438 LTWERVSQVDHVIWPDGRVLLAEGRLLNLSCSTVPTFLSTATTQALALIELVNA 497
QY 474 EGRYKQDVYLLPKMDEVVASHLPSPDAHLLTELTDQAKYLGNKNGPFKNYRY 530
DB 498 EGRYKQDVYLLPKMDEVVASHLPSPDAHLLTELTDQAKYMGINKNGPFKNYRY 554

RESULT 13
ID Q661PI_XENLA PRELIMINARY; PRT; 520 AA.
AC Q661PI_11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE MG86404 protein.
GN Name=MG86404;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;
OC Xenopodidae; Xenopus; Xenopus.

OX NCBI_TaxID=8355;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=2231132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.,
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (3)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RA Klein S., Gerhard D.S.;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonCommercial license
 CC -----
 CC EMBL: BC081269; AAH81269.1; -; mRNA.
 DR GO; GO:0004013; Fadenosylhomocysteine activity; IEA.
 DR GO; GO:0006730; P-one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad-hcy hydrolase.
 DR PANTHER; PTHR11784; Ad-hcy hydrolase; 1.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF06570; AdoHcyase; NAD; 1.
 DR TIGRfam; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 SQ SEQUENCE 520 AA; 57839 MW; C73583CP180234C3 CRC64;
 Query Match 88.4%; Score 2459; DB 2; Length 520;
 Best Local Similarity 87.4%; Pred. No. 8, 2e-183;
 Matches 464; Conservative 32; Mismatches 23; Indels 12; Gaps 3;
 OY 1 MSMPDMPPLPGVGEELKQAEDEAKYSFPAVATVAPKQKQIOPADDMOEFKPTKTR 60
 DB 1 MLPLPAV-----TDEPAALAKRFLFMAVSTKPPK-10FADDMGEFSKRTKTR 49
 OY 61 RLSRSISGSSSTDSYSAASYDSSDDEVSPEKQQTNSKSSNFCVKNIKQAEFERREI 120
 DB 50 RLSRSISGSSSTDSYSAASYDSSDDEVSPEKQQTNSKSSNFCVKNIKQAEFERREI 109
 OY 121 ELAEDMSALLSRKRAQGEKPLAGAKIYGCCTHTVLTOTVLETTLCALAQGWSACNY 180
 DB 110 DIAEDMSALLSRKRAQGEKPLAGAKIYGCCTHTVLTOTVLETTLCALAQGWSACNY 169
 OY 181 STONEVAALLAEAGVAVFAWKGESEDDFMWCIDRCVNM-D-GMANNILDDGDLTHVYK 239

DB 170 STONEVAALLAEAGVAVFAWKGESEDDFMWCIDRCVNMDSGQANNILDDGDLTHVYK 229
 OY 240 KYPNPFKIRGIVESVTGVHRLYOLSKAGKLCVPMNVNDSVTKQPDNLYCCRESILD 299
 DB 230 KYPNPFKIRGIVESVTGVHRLYOLSKAGKLCVPMNVNDSVTKQPDNLYCCRESILD 289
 OY 300 GLKRTDWMFGGKQVYVGVGVGGCCAAKALGAIYITIDIPICALQACMDGRVYK 359
 DB 290 GLKRTDWMFGGKQVYVGVGVGGCCAAKALGAIYITIDIPICALQACMDGRVYK 349
 OY 360 LNEVIRQVDVITTCGNKNVYREHLDRMKNSCIYCNMGHSTELDVTSLRTPETLWERY 419
 DB 350 LNEVIRQVDVITTCGNKNVYREHLDRMKNSCIYCNMGHSTELDVTSLRTPETLWERY 409
 OY 420 RSQVDHVPDGRVLLAEGRLNLSGCTVPTFVLSITATITQALALIELYNAPEGRYK 479
 DB 410 RSQVDHVPDGRVLLAEGRLNLSGCTVPTFVLSITATITQALALIELYNAPEGRYK 469
 OY 480 DYLLPDKMDVVASLHPSPDHLTELTDQAKYLGINKGPFKNRYR 530
 DB 470 DYLLPDKMDVVASLHPSPDHLTELTDQAKYLGINKGPFKNRYR 520
 RESULT 14
 ID SAH3_HUMAN STANDARD; PRT; 611 AA.
 AC Q96HN2; O94917;
 DT 11-JUL-2002, integrated into UniProtKB/Swiss-Prot.
 DT 01-DEC-2001, sequence version 1.
 DT 07-FEB-2006, entry version 26.
 DE Putative adenosylhomocysteine 3 (EC 3.3.1.1) (S-adenosyl-L-
 DE homocysteine hydrolase) (AdoHcyase).
 GN Name: KIA0828;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain;
 RX MEDLINE=99156230; PubMed=10048485; DOI=10.1093/dnares/5.6.355;
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XII.
 RT The complete sequences of 100 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 5:355-364(1998).
 RN (2)
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Lung, and Uterus;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-

homocysteine + adenosine.
-1- CORFACTOR: Binds 1 NAD per subunit (By similarity).
-1- PATHWAY: Activated methyl cycle.
-1- SIMILARITY: Belongs to the adenosylhomocysteine family.
Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
Distributed under the Creative Commons Attribution-NonDerivs License

EMBL, AB020635, BAA74851.1, ALT_INIT, mRNA.
EMBL, BC008349, AAH08349.1, -, mRNA.
EMBL, BC024325, AAH24325.1, -, mRNA.
HSSP, P23526, 1L14.
Ensembl, ENSG00000158467, Homo sapiens.
InterPro, IPR000043, Ad_hcy_hydrolase.
PANTHER, PTHR11784, Ad_hcy_hydrolase, 1.
Pfam, PF05221, AdoHcyase, 1.
Pfam, PF00670, AdoHcyase NAD, 1.
TIGRFAMs, TIGR00936, ahcy, 1.
DR PROSITE, PS00738, ADOHCYASE_1, 1.
DR PROSITE, PS00739, ADOHCYASE_2, 1.
Kw Hydrolase; NAD; One-carbon metabolism.
CHAIN 1 611
FT REGION 362 529 /FTid=PRO_0000116909.
FT BINDING 236 329 NAD binding (By similarity).
FT BINDING 310 310 Substrate (By similarity).
FT BINDING 335 335 Substrate (By similarity).
FT BINDING 365 365 Substrate (By similarity).
FT BINDING 369 369 Substrate (By similarity).
FT CONFLICT 122 122 Missing (in Ref. 1).
SQ SEQUENCE 611 AA; 66721 MW; A76B1275FC0DB91D CRC64;

Query Match 88.3%; Score 2456; DB 1; Length 611;
Best Local Similarity 84.9%; Pred. No. 1.8e-182;
Matches 468; Conservative 31; Mismatches 24; Indels 28; Gaps 3;

8 PLPGVGE-----ELKQAKIEDAEK-----SMATATKAP---K 39
61 FVPGGSGPPAALASPAAGVPAQASMKSSDPHHQHRHDEGALVSPDGTETPRVTK 120
40 KQIQPADDMOEFTEPTKTRRSLSRSISQSTDSYSSAAYTDSDEVSFPRKQNTS 99
121 KQIQPADDKQKQENKRPKTKGRSLRSISQSTDSYSSAAYTDSDEVSFPRKQNTS 180
100 KGSNFCYKNTKQAFGRREIFIAQDMSALISLKRQAGEKPLGAKIVGCTHTTAQTA 159
181 KGSNFCYKNTKQAFGRREIFIAQDMSALISLKRQAGEKPLGAKIVGCTHTTAQTA 240
160 VLIELTALGAQCRSACNIVYSTONEVAALAEAGVAPAMGSEDEDFMWCIDRCVME 219
241 VLIELTALGAQCRSACNIVYSTONEVAALAEAGVAPAMGSEDEDFMWCIDRCVME 300
220 GQOANMILDDGGDLTHWVYKKYPNFKKIRGIVGESVGVNHLVYLSRAGKLCVPMNVN 279
301 GQPMIILDDGGDLTHWVYKKYPNFKKIRGIVGESVGVNHLVYLSRAGKLCVPMNVN 360
280 DSVTKQKFDNLYCCRESILDDGKRTTDMVFGSKQYVVCYGEVGGCCALKALGAIYI 339
361 DSVTKQKFDNLYCCRESILDDGKRTTDMVFGSKQYVVCYGEVGGCCALKALGAIYI 420
340 TEIDPICALQCMDFRLVKNEVIRQVDIVTTCGNKNVYTRHLDPMKNSCIYCNNGH 399
421 TEIDPICALQCMDFRLVKNEVIRQVDIVTTCGNKNVYTRHLDPMKNSCIYCNNGH 480
400 SNTIEDVTSLSLPELTWERVRSQVHVIMPDGKRVLLAEGRLNLSCSTVPTFLSITA 459
481 SNTIEDVTSLSLPELTWERVRSQVHVIMPDGKRVLLAEGRLNLSCSTVPTFLSITA 540
460 TQOALALIELYNAPBGRYKQDVYLLPKKMDVVASLHPSFPAHLTELTDQAKYLGLNK 519
541 TQOALALIELYNAPBGRYKQDVYLLPKKMDVVASLHPSFPAHLTELTDQAKYLGLNK 600
520 NGPKENYRY 530

DB 601 NGPKENYRY 611
|||||
RESULT 15
068FL4 MOUSE PRELIMINARY; PRT; 613 AA.
ID 068FL4 MOUSE
AC 068FL4;
DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE RIKEN CDNA 4631427C17.
GN Name=4631427C17rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain; STRAIN=C57BL/6;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marutina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S.C., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schermer A., Schein J.E., Jones S.J.M., Watra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- CORFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
Distributed under the Creative Commons Attribution-NonDerivs License

EMBL, BC079660, AAH79660.1, -, mRNA.
Ensembl, ENSMUSG00000029772, Mus musculus.
MG1, MG1:1921590, 4631427C17rik.
DR GO, GO:0004013, F:adenosylhomocysteine activity, IEA.
DR GO, GO:0016787, F:hydrolase activity, IEA.
DR GO, GO:0006730, F:one-carbon compound metabolism, IEA.
DR InterPro, IPR000043, Ad_hcy_hydrolase.
DR PANTHER, PTHR11784, Ad_hcy_hydrolase, 1.
DR Pfam, PF05221, AdoHcyase, 1.
DR Pfam, PF00670, AdoHcyase NAD, 1.
DR TIGRFAMs, TIGR00936, ahcy, 1.
DR PROSITE, PS00738, ADOHCYASE_1, 1.
DR PROSITE, PS00739, ADOHCYASE_2, 1.
Kw Hydrolase; NAD; One-carbon metabolism.
SQ SEQUENCE 613 AA; 66899 MW; 4413DBF1F4825860 CRC64;

Query Match 88.2%; Score 2454; DB 2; Length 613;

Best Local Similarity 84.9%; Pred. No. 2,5e-182;
Matches 468; Conservative 30; Mismatches 25; Indels 28; Gaps 3;

```
QY      8 PLPGVGE-----ELKQAEIEDAEKY-----SFMATVTKAP---K 39
Db      63 PAFGPGSGPFAALSPAAGKVPQASAMKSPHNOHRDGGELALVSPDGTVEAPRTVK 122
QY      40 KOIQADDMQGEFTKFPPTKGRRSISRSISQSSDTSYSSAASYTSSDDEVSPREKQNTS 99
Db      123 KOIQADQKQEFNRPFKIGRRSISRSISQSSDTSYSSAASYTSSDDEVSPREKQNTS 182
QY      100 KGSNNFCVKNIKQAEFRREIEIAEQMSALISLRKQAGEKPLAGAKIVGCTHITAQTA 159
Db      183 KSSSDFCVKNIKQAEFRREIEIAEQMPALMRKQAGEKPLAGAKIVGCTHITAQTA 242
QY      160 VLIETLCALGAQCRMSACNIYSTONEVAALAAGVAVFAMKGESEDDFMWCIDRCVNM 219
Db      243 VLMETLCALGAQCRMAACNIYSTLINEVAALAESGFPVFAMKGESEDDFMWCIDRCVNE 302
QY      220 GWQANNILDDGDLTHWVYKKYPNVFKKIRGIIVESYTGVRLLYQLSKAGKLCVPAMNVN 279
Db      303 GWQPNMILDDGDLTHWYKKYPNMFKKIRGIIVESYTGVRLLYQLSKAGKLCVPAMNVN 362
QY      280 DSVTKQKFDNLVCCRESILDLKRTDVMFGKQVAVCGYGEVKGCCALKALGALVYI 339
Db      363 DSVTKQKFDNLVCCRESILDLKRTDMMFGKQVAVCGYGEVKGCCALKAMGSLVYV 422
QY      340 TEIDPICALQACMDGFRVVLNEVIROVDVITCTGNKNVTRERHLDPMKNSCIVCNMGH 399
Db      423 TEIDPICALQACMDGFRVVLNEVIROVDVITCTGNKNVTRERHLDPMKNSCIVCNMGH 482
QY      400 SNTIEDVTSIRTPELTWERVRSQVDHVIWPDGKRVLLAEGRLNLSCSTVPTFVLSTTA 459
Db      483 SNTIEDVASIRTPELTWERVRSQVDHVIWPDGKRIVLLAEGRLNLSCSTVPTFVLSTTA 542
QY      460 TTQALALIELYNAPBGRYKQDVYLLPKMDYVVASLHLPSFDAHLTELFDQAKYLGINK 519
Db      543 TTQALALIELYNAPBGRYKQDVYLLPKMDYVVASLHLPTFDAHLTELFDQAKYLGINK 602
QY      520 NGPFKPNYYRY 530
Db      603 NGPFKPNYYRY 613
```

Search completed: September 6, 2006, 19:29:38
Job time : 275.337 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:30:04; Search time 53 Seconds

(without alignments)
875,306 Million cell updates/sec

Title: US-10-683-610-1

Perfect score: 2781

Sequence: 1 MSMPAMPLPGVGEELKQAK.....QAKYGLNKGPFKNRYR' 530

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 650591 segs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /EMC_Celerra_SIDS3/ptodata/2/1aa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/1aa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/1aa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/1aa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/1aa/PCYUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2618	94.1	500	1	US-08-896-005-1
2	1819.5	65.4	504	1	US-08-896-005-3
3	1160	41.7	432	1	US-08-896-005-5
4	1151	41.4	432	1	US-08-896-005-4
5	1151	41.4	432	2	US-09-347-878-1
6	1150	41.4	432	2	US-09-546-013-3
7	1150	41.4	447	2	US-09-949-016-10359
8	1108	39.8	515	2	US-09-248-796A-18264
9	1099.5	39.5	476	2	US-09-902-540-10728
10	1086	39.1	485	2	US-08-930-894-2
11	1079.5	38.8	502	2	US-09-252-991A-23501
12	1074	38.6	498	2	US-09-919-854-2
13	1062	38.2	463	2	US-09-328-352-4600
14	1032	37.1	486	2	US-09-759-990A-7
15	409.5	14.7	387	2	US-09-489-039A-8393
16	322	11.6	68	2	US-09-270-767-33605
17	322	11.6	68	2	US-09-270-767-48822
18	313	11.3	99	2	US-08-930-894-8
19	216	7.8	139	2	US-08-930-894-6
20	211	7.6	97	1	US-08-204-740-7
21	211	7.6	97	2	US-09-081-167A-7
22	211	7.6	97	2	US-09-081-395-7
23	211	7.6	97	2	US-09-416-833-7
24	211	7.6	97	5	PCR-US95-02521-7
25	209.5	7.5	138	2	US-08-930-894-5
26	207.5	7.5	140	2	US-08-930-894-4

27	204	7.3	81	2	US-09-513-999C-5999	Sequence 5999, Ap
28	196.5	7.1	95	1	US-08-204-740-9	Sequence 9, Appl
29	196.5	7.1	95	2	US-09-081-167A-9	Sequence 9, Appl
30	196.5	7.1	95	2	US-09-081-395-9	Sequence 9, Appl
31	196.5	7.1	95	2	US-09-416-833-9	Sequence 9, Appl
32	196.5	7.1	95	5	PCR-US95-02521-9	Sequence 9, Appl
33	186	6.7	139	2	US-08-930-894-7	Sequence 7, Appl
34	112.5	4.0	416	2	US-09-543-681A-5020	Sequence 5020, Ap
35	106	3.8	1481	2	US-09-231-899-70	Sequence 70, Appl
36	105.5	3.8	539	2	US-09-489-039A-13875	Sequence 13875, A
37	105	3.8	760	2	US-09-489-039A-9113	Sequence 9113, Ap
38	101	3.6	783	2	US-09-540-236-2284	Sequence 2284, Ap
39	97	3.5	542	2	US-09-538-092-289	Sequence 289, App
40	97	3.5	1078	2	US-09-248-796A-20284	Sequence 20284, A
41	97	3.5	1409	2	US-09-949-001-22	Sequence 22, Appl
42	96.5	3.5	1432	2	US-08-781-891-71	Sequence 71, Appl
43	96.5	3.5	1432	2	US-09-618-166-71	Sequence 71, Appl
44	96.5	3.5	1432	2	US-09-949-001-16	Sequence 16, Appl
45	95.5	3.4	374	2	US-09-647-224A-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-896-005-1
Sequence 1, Application US/08896005
Patent No. 5854023
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,005
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0337 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
CLONE: 1519044
US-08-896-005-1
Query Match 94.1%; Score 2618; DB 1; Length 500;
Best Local Similarity 99.8%; Pred. No. 1,3e-287;

Matches	499: Conservative	0	Mismatches	1	Indels	0	Gaps	0
Qy	31	MATYTKAKKKQIQFADDMQOEFTKPTTKGRRLSLSSISQSSSTDSYSSAASYDSSDDSVS	90					
Db	1	MATYTKAKKKQIQFADDMQOEFTKPTTKGRRLSLSSISQSSSTDSYSSAASYDSSDDSVS	60					
Qy	91	PREKQOTSKSGSSNFCVKNIKQAEFGREIEIAEQDMSALISLRKRAQEKPLAKIVG	150					
Db	61	PREKQOTSKSGSSNFCVKNIKQAEFGREIEIAEQDMSALISLRKRAQEKPLAKIVG	120					
Qy	151	CTHTTAQTAVALIETLCALGAOCRWASACNIYSTQNEVAALAEAGVAVPAWKGESEDDPFW	210					
Db	121	CTHTTAQTAVALIETLCALGAOCRWASACNIYSTQNEVAALAEAGVAVPAWKGESEDDPFW	180					
Qy	211	CIDRCVNNDDGQOANMLIDDGGDLTMVYKKPKNVFKKIRGIIEESVTVGHRLYOLSKAGK	270					
Db	181	CIDRCVNNDDGQOANMLIDDGGDLTMVYKKPKNVFKKIRGIIEESVTVGHRLYOLSKAGK	240					
Qy	271	LCVPANVNDSVTKOKFENLYCCRESILIDGLKRTTDMVFGKQVAVGCGYGEVKGCCAL	330					
Db	241	LCVPANVNDSVTKOKFENLYCCRESILIDGLKRTTDMVFGKQVAVGCGYGEVKGCCAL	300					
Qy	331	KALGAIVYTEIDPICALOACMDGSRVYKLNVEIRQDVVITCTGNKVYVREHIDRAKN	390					
Db	301	KALGAIVYTEIDPICALOACMDGSRVYKLNVEIRQDVVITCTGNKVYVREHIDRAKN	360					
Qy	451	PTFVLSTATTQALALIELYNAPBGRYKQDYVYLPFKRNDVYASLHLSFDAHLTELTD	510					
Db	421	PTFVLSTATTQALALIELYNAPBGRYKQDYVYLPFKRNDVYASLHLSFDAHLTELTD	480					
Qy	511	QAKYLGKNGPFPKNYYRY 530						
Db	481	QAKYLGKNGPFPKNYYRY 500						

RESULT 2
US-08-896-005-3
Sequence 3, Application US/08896005
Patent No. 5854023
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PasteSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,005
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0337 US
TELECOMMUNICATION INFORMATION:

[illegible]

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0337 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 904132
;
US-08-896-005-5

Query Match          41.7%; Score 1160; DB 1; Length 432;
Best Local Similarity 51.8%; Pred. No. 3.4e-122;
Matches 220; Conservative 83; Mismatches 120; Indels 2; Gaps 2;

107 VKNIKQAEFGREIEIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLC 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
9 VADIGLAMGKALDIENEMPGIMRMRERYSASKPLGARIAGCLHMTVETAVLIETLV 68

167 ALGAQCRMSACNIYSTONEVAALAEAGVAVFAMKGESEDFWMCIDRCVMMDGQAMNI 226
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 ALGAEVWSSCNISTQDHAAALAKAGIPYFAMKGETDEEYLCIEOTLFFKQGPLNMI 128

227 LDDGGDLTHWYKKYKPNVFKKIRGIVESVGVHLYQLSKAGKLCVPMNVNDSVTXK 286
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
129 LDDGGDLTNLIHTKIPOLLGIRGISEETTTGVHLYKMMANGILNVPAINVDSVTXK 188

287 FDNLYCCRESILDLGKRTTDMFGKQOVVCGYGVGKCCALKALGAIYITEIDPIC 346
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
189 FDNLYCCRESILDLGKRTTDMFGKQOVVCGYGVGKCCALKALGAIYITEIDPIC 248

347 ALQACMGDFRYVKLNEVIRQDVVITCTGNKNAVTRHLDKMKSCIVCMNGHSTETIDV 406
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
249 ALQACMGDFRYVKLNEVIRQDVVITCTGNKNAVTRHLDKMKSCIVCMNGHSTETIDV 308

407 TSLRTPELTWERVRSQVDHVIMPDGKRVLLAEGRLNLSCST-VPTFVLSTATTOALA 465
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 KMLNENAVEKNVIRQVDVRYLKNGRRIILAEGLVNLGCMGHPSPVMSNFTNQVMA 368

466 LIEILYNAPEGRYKQDVYLLPKKMDYVVASLHLPFDAHTELTDQAKYGLKNKGPFPK 525
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 QIELMTWHPD-KYRPGVHFLPKKIDBAVAEAHLGKLNVLTKLTETKQAOYLGMPINGPFPK 427

QY 526 NYRYR 530
   :|||
DB 428 DHYRY 432

RESULT 4
; Sequence 4, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0337 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 432 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 178277
;
US-08-896-005-4

Query Match          41.4%; Score 1151; DB 1; Length 432;
Best Local Similarity 51.3%; Pred. No. 3.6e-121;
Matches 218; Conservative 85; Mismatches 120; Indels 2; Gaps 2;

107 VKNIKQAEFGREIEIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLC 166
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
9 VADIGLAMGKALDIENEMPGIMRMRERYSASKPLGARIAGCLHMTVETAVLIETLV 68

167 ALGAQCRMSACNIYSTONEVAALAEAGVAVFAMKGESEDFWMCIDRCVMMDGQAMNI 226
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
69 ALGAEVWSSCNISTQDHAAALAKAGIPYFAMKGETDEEYLCIEOTLFFKQGPLNMI 128

227 LDDGGDLTHWYKKYKPNVFKKIRGIVESVGVHLYQLSKAGKLCVPMNVNDSVTXK 286
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
129 LDDGGDLTNLIHTKIPOLLGIRGISEETTTGVHLYKMMANGILNVPAINVDSVTXK 188

287 FDNLYCCRESILDLGKRTTDMFGKQOVVCGYGVGKCCALKALGAIYITEIDPIC 346
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
189 FDNLYCCRESILDLGKRTTDMFGKQOVVCGYGVGKCCALKALGAIYITEIDPIC 248

347 ALQACMGDFRYVKLNEVIRQDVVITCTGNKNAVTRHLDKMKSCIVCMNGHSTETIDV 406
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
249 ALQACMGDFRYVKLNEVIRQDVVITCTGNKNAVTRHLDKMKSCIVCMNGHSTETIDV 308

407 TSLRTPELTWERVRSQVDHVIMPDGKRVLLAEGRLNLSCST-VPTFVLSTATTOALA 465
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
309 KMLNENAVEKNVIRQVDVRYLKNGRRIILAEGLVNLGCMGHPSPVMSNFTNQVMA 368

466 LIEILYNAPEGRYKQDVYLLPKKMDYVVASLHLPFDAHTELTDQAKYGLKNKGPFPK 525
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
369 QIELMTWHPD-KYRPGVHFLPKKIDBAVAEAHLGKLNVLTKLTETKQAOYLGMSCDGPFKP 427

QY 526 NYRYR 530
   :|||
DB 428 DHYRY 432

RESULT 5
```


US-09-949-016-10359

Query Match 41.4%; Score 1150; DB 2; Length 447;

Best Local Similarity 48.7%; Pred. No. 5e-121;

Matches 223; Conservative 89; Mismatches 126; Indels 20; Gaps 3;

QY 74 SVSSAASATYSSDDDEVSPPREKOOTNSKSSNFCVKNIKAEFGREIEIAEDOMSLISL 133

DB 9 STTSAASMSDKLP-----YKVAIDIGLAAMGRKALDIAENMPEGLMM 50

QY 134 RRAOGEKPLAGAKIVGCTHITAQTAVLIETLICALGACRMSACNIYSTONEVAALAE 193

DB 51 KERYASAKPLKARLAGCMLHMTVEITAVLIETLVLTGAEVQSSCNIFSTQDHAALAAIA 110

QY 194 GVAFAWKGESDEDDFWCICIDRCVNMDGMOANNILDDGDLTHWVYKRYNVEKRIIGIVE 253

DB 111 GIPVAMKGETDEBEYLMCIETGLYFADGDLNMLIDDGDDLTHWVYKRYNVEKRIIGIVE 170

QY 254 ESVTVGNHLVYLSKAGKLCVPMANNVNDSTYKOKFNLVCCRESILDLKRTTDVWFGKQ 313

DB 171 ETTTGVNHLVYKMMANGILKVPAINVNDSTYKOKFNLVCCRESILDLKRTTDVWFGKQ 230

QY 314 VVCGYGEVKGCCCAALKALGAIYVITEIDPICALQACMDGFRVYKLVNEVIRQVAVITC 373

DB 231 AVVAGYGVGKCCCAALKALGAIYVITEIDPICALQACMDGFRVYKLVNEVIRQVAVITC 290

QY 374 TGNKNVVTREHLDRMKNSCIVCMGHSNTEIDVTSLRPELTWERVRSQVDHVIWPDGR 433

DB 291 TGCIDIIILGRHEQKKDPAIVCNIGHFVEIDVKNLNEVAEKVNIKPQVDRYLKNGR 350

QY 434 VVLAEGSLNLSCST-VPTFLSTATTQALALIELYAPGRKQODYLLPKMDEV 492

DB 351 ILLAEGSLNLSCST-VPTFLSTATTQALALIELYAPGRKQODYLLPKMDEV 409

QY 493 ASLHPSFDAHLTELTDQAKYLGNKNGPFKNYRY 530

DB 410 AEHLGKLVNKLTKTEKQAQYLGMSCDGPFKPDHRY 447

RESULT 8

US-09-248-796A-18264

Sequence 18264, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18264

LENGTH: 515

TYPE: PRT

ORGANISM: Candida albicans

US-09-248-796A-18264

Query Match 39.8%; Score 1108; DB 2; Length 515;

Best Local Similarity 49.0%; Pred. No. 3.8e-116;

Matches 220; Conservative 86; Mismatches 127; Indels 16; Gaps 4;

QY 98 NSKGSNFCVKNIKAEFGREIEIAEDOMSLISLRKRAOGEKPLAGAKIVGCTHITRQ 157

DB 67 SSAAPTNTKVAIDISLAAGRKDIELSENMPEGLMIRKYYGSPQPKARLAGCMLHTIQ 126

QY 158 TAVLIETICALGACRMSACNIYSTONEVAALAEAGVAVFAMKGESEDDFWCICIDR--C 215

DB 127 TAVLIETICALGAEVYMSCNIFSTQDHAALAAIAAGVAVFAMKGETDEBEYLMCIETGL 186

US-09-902-540-10728

Sequence 10728, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 10728

LENGTH: 476

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-10728

QY 216 VMDGMOANNILDDGDLTHWVYKRYNVEKRIIGIVEBSVTVGNHLVYLSKAGKLCVPA 275

DB 187 AFKDDKLNILDDGDLTSLVHERYPEMLBEDCYGLSEBTGTVHHLVYLSKAGKLCVPA 246

QY 276 MNVNDSTYKOKFNLVCCRESILDLKRTTDVWFGKQVWVCGYGEVKGCCCAALKALG 335

DB 247 INVNDSTYKOKFNLVCCRESILDLKRTTDVWFGKQVWVCGYGEVKGCCCAALKALG 306

QY 336 IYVITEIDPICALQACMDGFRVYKLVNEVIRQVAVITCTGNKNVVTREHLDRMKNSCIVC 395

DB 307 RYVITEIDPICALQAAVGYQVAPMDEVASIGQIFVTTGCRDITTGKHFQMPPEHALVC 366

QY 396 NMGHSNTEIDVTSLRPELTWERVRSQVDHVIWPDGRVLLAEBRLNLSCST--VPTFV 454

DB 367 NIGFPIEDIVAMLIANESVNIKIPQVDRYLMKGRHVLILADGRVLNLCGATGHSFV 426

QY 455 LSTITQALALIELYNA-----PE-----GRKQDYLLPKMDEVYASLHLPSEF 501

DB 427 MSCFSNOVLQIALFNADNKEFREKPEFAKTFGPFVGVHLLPKVLDVETARCLHDHIG 486

QY 502 AHLTELTDQAKYLGKNGPFKNYRY 530

DB 487 AKLTLETQAEVYLGIPESPYKADYRY 515

RESULT 9

US-09-902-540-10728

Sequence 10728, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 10728

LENGTH: 476

TYPE: PRT

ORGANISM: Myxococcus xanthus

US-09-902-540-10728

Query Match 39.5%; Score 1099.5; DB 2; Length 476;

Best Local Similarity 47.0%; Pred. No. 3e-115;

Matches 220; Conservative 82; Mismatches 123; Indels 43; Gaps 5;

QY 104 NFCVKNIKAEFGREIEIAEDOMSLISLRKRAOGEKPLAGAKIVGCTHITAQTAVLIE 163

DB 11 DYALADSLADWKGKEIRIAESEMPALMAIREYAKTQPLGARTGSLHMTIOTAVLVE 70

QY 164 TLICALGACRMSACNIYSTONEVAALAEAGVAVFAMKGESEDDFWCICIDRVM----- 218

DB 71 TLQALGAEVRWASCNIFSTQDHAALAAVQAGTPVFAHKGESLKEWDFTHRIFDGPAGS 130

QY 219 DGMQANNILDDGDLTHWV--KK-----YFN 243

DB 131 DHEGPMILDDGDLTSLVHERYPEMLBEDCYGLSEBTGTVHHLVYLSKAGKLCVPA 190

QY 244 VFKKIRGIVESVTVGNHLVYLSKAGKLCVPMANNVNDSTYKOKFNLVCCRESILDLGK 303

DB 191 KSAITLSTETTTGTVHRLQEMSAKGTLLFPRAIVNDSVTSKFNLVCCRESILDLGK 250

QY 304 TTVWFGKQVWVCGYGEVKGCCCAALKALGAIYVITEIDPICALQACMDGFRVYKLVNEV 363

DB 251 ATDVWVAGKIVVAGYGVGKSAQALRALSAQVWVTEIDPICALQAAAMEGRVVTMDYA 310

QY 364 IROYDVVITCTGNKNVVTREHLDRMKNSCIVCMGHSNTEIDVTSLRPELTWERVRSQV 423

Db 311 ADKADIFVATGNKGVITHDHMAKMDQAIVCNIGHFDNEIEVASLE--KYKMEIKPOV 368
QY 424 DHVIMPDGKRVLLAEGRLLNLSCST-VPTFVLSTATTQALALIELYNAPESGRYKODY 482
Db 369 DHIIIFPNKRIILLAGRLVNLGCGTGHPSYVSSSPANQTIQIELYSHSANYEVGKYV 428
QY 483 LRPKMDVEYASHLPSFDAHLTEITDDQAKYIUGLNKGPFKNRYR 530
Db 429 VLPKHLDEKVALQLKLNALQTELSEQADYIGVKTSGPKDYRY 476

RESULT 10

US-08-930-894-2
Sequence 2, Application US/08930894
Patent No. 6037524
GENERAL INFORMATION:
APPLICANT: GREENLAND, Andrew James
APPLICANT: DRAPER, John
APPLICANT: SKIPSEY, Marc
APPLICANT: WARNER, Simon
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOTER
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,894
FILING DATE: 09-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/00882
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9507381.3
FILING DATE: 10-APR-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-930-894-2

Query Match 39.1%; Score 1086; DB 2; Length 485;
Best Local Similarity 45.7%; Pred. No. 1,1e-113;
Matches 225; Conservative 84; Mismatches 125; Indels 46; Gaps 6;
QY 107 VKNIKQAEFGREIEIAEODMSALILKRAQGEKPLAGAKIVGCTHITTAQIVLIETTC 166
Db 16 VDMQADGRLEIEIAEVEPMGIMACRAEFGRAPGPKAKITGSIHMTIQTAVLIETTL 75
QY 167 ALGAOCRWKACNISTYQNEVAALAEAGYAVFAMKGESEDDFWWCIDRCVNM-DGQAM 225
Db 76 ALGPEFRKSCNIFSTQDHAALAIARDASVFAMKGETLOEYIMWCTERALDMPGCGPDI 135
QY 226 ILDDGGDLTHWYK-----KYPNV 244
Db 136 IYDDGGDTLLIHEGVKABEEVEKGTGMPDPASTDAEFOIVLTIIRDGLKVDPTXRYM 195
QY 245 FKIKRIVEASTYGVHRLYQLSKAGKLCVPANVNDSTVKQKDNLYCCRESILDGAKT 304
Db 196 KRIYGVSEETITGVKRLYQOMANNSILFPAINVNDSTVSKSPDNLYGGRHSILPDILMRA 255
QY 305 TDVIMFGKQVNVGVGEVKGCCALKALGAIYIITEIDICALQCMGDFRVVVKLNEVI 364

Db 256 TIVMIAKGAIVVCGVGDVGECAALKQAGARIVITEIDICALQALMEGLVLTLEDV 315
QY 365 ROVDVITCTGNKNVYTRREHLDNRKNSCIVCNMGHSNTEIDVTSRT-PELTWERYSCV 423
Db 316 SEADIFVITTGKNDILMDHMKMKONALVCNIGHFDNEIDMLGLETYPGIRITIKPOT 375
QY 424 DHVIMPD-GKRVLLAEGRLLNLSCST-VPTFVLSTATTQALALIELYN-APESGRYKOD 480
Db 376 DRWVFPETITGIIVLAEGRLNMLGCATGHPFVMSCSFTNQVIAOLEMNEKASGKEYEK 435
QY 481 VYLLPKMDVEYASHLPSFDAHLTEITDDQAKYIUGLNKGPFKNRYR 530
Db 436 VYLPKHLDEKVALQLKLNALQTELSEQADYISVLEPGYKPEHRY 485

RESULT 11

US-09-252-991A-23501
Sequence 23501, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23501
LENGTH: 502
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23501

Query Match 38.8%; Score 1079.5; DB 2; Length 502;
Best Local Similarity 45.1%; Pred. No. 6.2e-113;
Matches 225; Conservative 93; Mismatches 144; Indels 37; Gaps 9;
QY 65 RSISSSTDSYSSASAYTDSDDSEVPREKQOTNSKGSNFCVKNIKQAEFGREIEIAE 124
Db 8 RALRPASPVCCQRTNGASHQTTNGEL--RMSAVMTAGTIDYKIVADITLLAMGRRELIIE 65
QY 125 QDMSALISLRKQAGEKPLAGAKIVGCTHITTAQIVLIETTCALGAOCRWKACNISTYQ 184
Db 66 SEMPALMGRKRYAGQGPLKAGKILGCIHMTIQTAVLIETTLVLAABYRWSSCNIFSTQD 125
QY 185 EVAALAEAGYAVFAMKGESEDDFWWCIDRCVNM-DG--WQANMILDDGGDLTHWYKYP 242
Db 126 QAAAIAAAGIFVFAMKGETEEYEMCIEQTLIKDGFWDNMVLDGGDLTEILAKKYP 185
QY 243 NVFKIRGIVESYGVHRLYQLSKAGKLCVPANVNDSTVKQKDNLYCCRESILDGK 302
Db 186 QLESRIHGTTEITGVHRLDMLKNGALKYPAINVNDSTVSKSDNLYGGRHSILDAIK 245
QY 303 RTDVMFGKQVNVGVGEVKGCCALKALGAIYIITEIDICALQCMGDFRVV-- 359
Db 246 RQTHLLSGKQALVIGYGDVGKSSQSLRQEGMIVKVAEVDPICAMQACMDGFEVYSPYK 305
QY 360 --LNE-----VIRQVDVITCTGNKNVYTRREHLDNRKNSCIVCNMGHSNTEIDVTS 408
Db 306 NGINDGTASIDAALLGIDILVITTVGNVNCVANMLALKKRAVVCNIGHFDNEIDTAF 365
QY 409 IRTPELTWERYSCVVDHYIWPDK-----RVLLAEGRLLNLSCST-VPTFVLST 458
Db 366 NR-KYMANBEYKPOV-KHIIHRTGKDGFPANHDYIILAEGRVNLVNGATGHPRSIMDS 423
QY 459 ATTQALALIELYN-----APESGRYKODVYLLPKMDVEYASHLPSFDAHLTEITDDQ 511
Db 424 FANQVLAQIHLFEGQKADLPAAEKAKRLSVEVLPKGLDEEVALBWKVFGGVVQTLTPKQ 483

QY 512 AKYLGNKNGPKPKNYRY 530
 Db 484 AEYIGVSGPFPKPDYRY 502

RESULT 12
 US-09-919-854-2
 / Sequence 2, Application US/0919854
 / Patent No. 6759224
 / GENERAL INFORMATION:
 / APPLICANT: FARMICK, MIKE
 / APPLICANT: HUTMACHER, KLAUS
 / APPLICANT: BREHME, JENNIFER
 / APPLICANT: PFEFFERLE, WALTER
 / APPLICANT: BINDER, MICHAEL
 / APPLICANT: GREISSINGER, DIETER
 / APPLICANT: THIERBACH, GEORG
 / TITLE OF INVENTION: Nucleotide sequences which code for the sahH gene
 / FILE REFERENCE: 211739USOX
 / CURRENT APPLICATION NUMBER: US/09/919,854
 / CURRENT FILING DATE: 2002-12-30
 / PRIOR APPLICATION NUMBER: DE 100 44 706.6
 / PRIOR FILING DATE: 2000-09-09
 / PRIOR APPLICATION NUMBER: DE 101 09 685.2
 / PRIOR FILING DATE: 2001-02-28
 / PRIOR APPLICATION NUMBER: US 60/294,277
 / PRIOR FILING DATE: 2001-05-31
 / NUMBER OF SEQ ID NOS: 4
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO 2
 / LENGTH: 498
 / TYPE: PRT
 / ORGANISM: Corynebacterium glutamicum
 US-09-919-854-2

Query Match 38.6%; Score 1074; DB 2; Length 498;
 Best Local Similarity 45.4%; Pred. No. 2,6e-112;
 Matches 215; Conservative 86; Mismatches 125; Indels 48; Gaps 5;

QY 104 NCFVKNIKOAEFGREIEIAEODMSALISLRKRAOGEKPLAGAKIVGCTHTTAQTAVLI 163
 Db 26 DFKVADLSLAEGRGRIQIRLAIEYEMPGMLQRFADQPLKGRIRLAGSIHMTVQRAVLIE 85
 QY 164 TLGALGAOCRSACNIYSTONEVAALA-----EAGVAVFAMKGESEDDFWMCIDRC 215
 Db 86 TLGALGAERWASCNIFSTQDEAAAIIVGSGTVEBPAGVPFAMKGESELEMYWCINQI 145
 QY 216 VAMDMQAMNIIIDGGDLTHMYK----- 239
 Db 146 FSWGDELPMIIDDGGDAMAVIRGEYEQAGLVPPAEANDSEYIAFLGMLREYLAAP 205
 QY 240 -KYRNVFKIRGIVESVTVGRVLYOLSKAGKLCVPMNVNDSYTKOKPDNLCCRESIL 298
 Db 206 GKMGKIAEYKVTETTTGVRHLTHFAEGVLPFPAMNVNDAVTKSKPDNKGTRHSIL 265
 QY 299 DGLKTTTVMFGKQVNVGCGYGEVGGCCCAALKALGAIYITETIDPICALQACMDGFRV 358
 Db 266 DGINRATMLMGKQVNLVCGYGVGKCAEAFDGGGARVKYTEADPINALQALMDGYSV 325
 QY 359 KLINEYIROVDVITCTGNKAVTTRHLDRMKSICVCMNGSHNTEIDVTS-LRTETLWE 417
 Db 326 TVDEAIEADAIYITATGNKDIIISFEQMLMKDHALGNGHFDNETDMHSLHRDVTRT 385
 QY 418 RYRSVDVHYWMDGRVVLAAEGRLLNLSCST-VPTFVLSTATTQALALIELYNAPEG 476
 Db 386 TIKPVDDETSTGSIIVLSBGRLLNLGNATGHSFVMSNSFAOQTIAQILEFQ-NEGQ 444
 QY 477 KYQDYLLPKNDYVVASLHPSFDAHLTELTDQAKYLGNKNGPKPKNYRY 530
 Db 445 YENEYRLPKVLDENKARHVEALGGQLTELKQEAIEYGVADVAGPFEKHEHYR 498

RESULT 13
 US-09-328-352-4600
 / Sequence 4600, Application US/09328352
 / Patent No. 6562958
 / GENERAL INFORMATION:
 / APPLICANT: Gary L. Breton et al.
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 / FILE REFERENCE: GTC99-03PA
 / CURRENT APPLICATION NUMBER: US/09/328,352
 / CURRENT FILING DATE: 1999-06-04
 / NUMBER OF SEQ ID NOS: 8252
 / SEQ ID NO 4600
 / LENGTH: 463
 / TYPE: PRT
 / ORGANISM: Acinetobacter baumannii
 US-09-328-352-4600

Query Match 38.2%; Score 1062; DB 2; Length 463;
 Best Local Similarity 47.6%; Pred. No. 5,2e-111;
 Matches 216; Conservative 84; Mismatches 126; Indels 28; Gaps 6;

QY 103 SNFCVKNIKOAEFGREIEIAEODMSALISLRKRAOGEKPLAGAKIVGCTHTTAQTAVLI 162
 Db 12 TDYKADISLADYGRKEIKLAEMPALIGRKRYAASKPLAGAKILGICHTTITQAVLI 71
 QY 163 ETLGALGAOCRSACNIYSTONEVAALAIEAGVAVFAMKGESEDDFWMCIDRCVNDG-- 220
 Db 72 ETLVGLAEVWTSNIFSTQDHAAAIARGIIPVFAKGETEYEVYVCEQIINVNGOP 131
 QY 221 WQAMNIIIDGGDLTHMYKVKYKPNVFKIRGIVEVSVTVHLYOLSKAGKLCVPMNVND 280
 Db 132 WDANMIIIDGGDLTALVHEKYPALERIGHTEETTVQRIEMKQGTLPAINVND 191
 QY 281 SVTKQFNLVCCRESIDGLKRTDVMFGKQVNVGCGYGEVGGCCCAALKALGAIYIT 340
 Db 192 SVTKSKDNKTKGCHRSNLDAIKRATDMLSRRLALVIGDVGKSAQSLRQEGNIVRT 251
 QY 341 EIDPICALQACMDGFRVYK-----LNEVYIROVDVITCTGNKAVTTRHLD 386
 Db 252 EVDPICAMQACMDGFEVSPYKNGVQTSKEDINHDLGNTDLVYTTGNGYHVCDAAMD 311
 QY 387 RMKNSCIYCMNGSHNTEIDVTSLRTPELTWERYRSQVDHVIWPDOK--VYVLAEGRLN 444
 Db 312 SLKAGAVVCNIGHFTEIDTAYLR--GYKWEVVKPQVQVRSQEDNNYILLSGRLVN 369
 QY 445 LSCST-VPTFVLSTATTQALALIELYN-----APEGRKYQDYLLPKNDYVVASLH 496
 Db 370 LGNATGHSRVMDSFANQVUGQIHLFQEKFPADLPASKAKIRYEVLPKULDEVAAAM 429
 QY 497 LPSPDAHLTELTDQAKYLGNKNGPKPKNYRY 530
 Db 430 VAGFGVLTQLTOBOADYLGIAVEGPFKSDAVKY 463

RESULT 14
 US-09-759-990A-7
 / Sequence 7, Application US/09759990A
 / Patent No. 6713273
 / GENERAL INFORMATION:
 / APPLICANT: Anticancer, Inc.
 / APPLICANT: Xu, Mingxu
 / TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGN
 / TITLE OF INVENTION: SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLMETHIONINE (SAM)
 / FILE REFERENCE: 31276-20026.00
 / CURRENT APPLICATION NUMBER: US/09/759,990A
 / CURRENT FILING DATE: 2001-01-12
 / PRIOR APPLICATION NUMBER: US 60/176,444
 / PRIOR FILING DATE: 2000-01-14
 / NUMBER OF SEQ ID NOS: 7
 / SOFTWARE: FastSeq for Windows Version 4.0

```

; SEQ ID NO 7
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-990A-7

```

Query Match	37.1%;	Score 1032;	DB 2;	Length 486;
Best Local Similarity	44.4%;	Pred. No. 1.5e-107;		
Matches 210;	Conservative 83;	Mismatches 130;	Indels 50;	Gaps 7;

```

Qy      107 :KXN:KQAEFFREIE:IAODMSALL:SLKRAQGEKRLAK:IVGCH:IAQTVL:ETLC 166
Db      15  IAD:INH:LGRKEL:LAEMPG:LVLR:RRYSAS:KPLKVR:ISGS:LMV:QVRA:VLE:ETL 74
Qy      167 ALGAOCRSACNIYSTONEVAALA-----EAGVAVFMWGESEDDFMWCIDRCYN 217
Db      75  ALGADVWASCNIFSTODTAAAIIVGPTYEPEKAGIPVFAMKGETTLEPEYMENTFRALT 134
Qy      218 M-DQMAMNIDDDGDLTHMVYKY-----PWFYFK----- 247
Db      135 WPDQGGPQVDDGGDALTLISKGFEPTAGAVPEPTENDNEYRCVATLTKQVFIQDGN 194
Qy      248 -----IRGIVESVTVHRLYOLSKRAGKLCVPMNVNDSVTKQFBNLYCCRESILD 299
Db      195 HMHTVAAGMNVSEETTTGVHRLYOLEKEGKLLFPAIVNDVAVTKSFNIVGCRSLID 254
Qy      300 GLKRTTDMPEGKQVNVCGYGEVGGCCALALALAIYITETIDPLCAQACMDGRYVK 359
Db      255 GINASDVMIGGKTALVMGYGVDGKGCAOSLFGOGGARVITIELDPLCAQOAMNEGVOVER 314
Qy      360 LNEVIRQDVVITCTGNKVVYREHLDRMKSNCIVCNMHSHSTELDVTSL-RTPELTWER 418
Db      315 IEEVVKVDIVTCTGNCNDIISVDMAQMKDAIYGNIGHFNEIDTDDGLMKYPGIKHLP 374
Qy      419 VRSGVDHVIWPDGKRVLLIABGRLLNLSCT-VPTFVLSTATTQALALIELYNABERY 477
Db      375 IKPEYDMWEPFDGHAILLIABGRLLNLGCAITGHPFSVMSSMSTNQTALQDILEY-KRGWL 433
Qy      478 KODVYLLPKKMDVYASLHPSFDAHLTELTDOKKYGLNKGNGPCKPMYUY 530
Db      434 EKQVYTLPKHLDEEVARLHLSLDVHLTKLTKQADYINVPPEGGYSPAYR 486

```

```

RESULT 15
US-09-489-039A-8393
; Sequence 8393, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8393
; LENGTH: 387
; TYPE: PRF
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-8393

```

Query Match	14.7%	Score 409.5;	DB 2;	Length 387;
Best Local Similarity	31.9%	Pred. No. 4.6e-37;		
Matches 119; Conservative	61;	Mismatches 170;	Indels 23;	Gaps 9;

[illegible][illegible]

Search completed: September 6, 2006, 19:32:22
Job time : 55 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:51:30 / Search time 176.283 Seconds
(without alignments)
1392.672 Million cell updates/sec

Title: US-10-683-610-1
Perfect score: 2781
Sequence: 1 MSMDAMPLEPGVGBELKQAK.....QAKYLGLNKGPFRKNRYRY 530

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published Applications AA Main:

- 1: /EMC_Celextra_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB.pap:*
- 2: /EMC_Celextra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pap:*
- 3: /EMC_Celextra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pap:*
- 4: /EMC_Celextra_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pap:*
- 5: /EMC_Celextra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pap:*
- 6: /EMC_Celextra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2781	100.0	530	US-10-876-285-2	Sequence 2, Appli
2	2781	100.0	530	US-10-876-285-4	Sequence 4, Appli
3	2781	100.0	530	US-10-876-285-6	Sequence 6, Appli
4	2781	100.0	530	US-10-683-610-1	Sequence 1, Appli
5	2781	100.0	614	US-09-782-051-2	Sequence 2, Appli
6	2781	100.0	614	US-11-110-748-2	Sequence 2, Appli
7	2778	99.9	530	US-10-876-285-8	Sequence 8, Appli
8	2449.5	88.1	519	US-10-756-149-5569	Sequence 5569, Ap
9	2429	87.3	564	US-10-467-903-1	Sequence 1, Appli
10	1970	70.8	521	US-11-097-143-2781	Sequence 2781, Ap
11	1819.5	65.4	504	US-11-097-143-41922	Sequence 41922, A
12	1601.5	57.6	455	US-10-450-763-42388	Sequence 42388, A
13	1289	46.4	426	US-10-369-493-10135	Sequence 10135, A
14	1187	42.7	461	US-10-369-493-4783	Sequence 4783, Ap
15	1187	42.7	461	US-10-369-493-7543	Sequence 7543, Ap
16	1185	42.6	463	US-10-369-493-19704	Sequence 19704, A
17	1158	41.6	466	US-10-369-493-12110	Sequence 12110, A
18	1154.5	41.5	432	US-11-097-143-39477	Sequence 39477, A
19	1152	41.4	499	US-11-079-463-7902	Sequence 7902, Ap
20	1151.5	41.4	457	US-09-925-301-1059	Sequence 1059, Ap
21	1151	41.4	432	US-10-836-953-1	Sequence 1, Appli
22	1145.5	41.2	433	US-10-435-802-4	Sequence 4, Appli
23	1142	41.1	461	US-10-369-493-11466	Sequence 11466, A
24	1142	41.1	461	US-10-369-493-14652	Sequence 14652, A
25	1142	41.1	461	US-10-369-493-21032	Sequence 21032, A
26	1142	41.1	464	US-10-369-493-15125	Sequence 15125, A
27	1141	41.0	437	US-10-369-493-5097	Sequence 5097, Ap

28	1132	40.7	485	4	US-10-767-701-47244	Sequence 47244, A
29	1129	40.6	433	4	US-10-369-493-2425	Sequence 2425, Ap
30	1129	40.6	433	4	US-10-369-493-2430	Sequence 2430, Ap
31	1127	40.5	466	4	US-10-369-493-8750	Sequence 8750, Ap
32	1126	40.5	447	4	US-10-369-493-3683	Sequence 3683, Ap
33	1126	40.5	469	4	US-10-314-657-71	Sequence 71, Appl
34	1126	40.5	469	5	US-10-473-193-71	Sequence 71, Appl
35	1125	40.5	463	4	US-10-369-493-20829	Sequence 20829, A
36	1118	40.2	428	4	US-10-369-493-10445	Sequence 10445, A
37	1117	40.2	465	4	US-10-369-493-17934	Sequence 17934, A
38	1111	39.9	485	4	US-10-156-761-12587	Sequence 12587, A
39	1110	39.9	476	4	US-10-369-493-8266	Sequence 8266, Ap
40	1106	39.8	463	4	US-10-369-493-16776	Sequence 16776, A
41	1105	39.7	449	4	US-10-369-493-1740	Sequence 1740, Ap
42	1105	39.7	463	4	US-10-369-493-7922	Sequence 7922, Ap
43	1099.5	39.5	466	4	US-10-369-493-19391	Sequence 19391, A
44	1097	39.4	459	4	US-10-369-493-10671	Sequence 10671, A
45	1085	39.0	468	4	US-10-369-493-9241	Sequence 9241, Ap

ALIGNMENTS

RESULT 1									
US-10-876-285-2									
Sequence 2, Application US/10876285									
Publication No. US20050044582A1									
GENERAL INFORMATION:									
APPLICANT: Kato, Masato									
APPLICANT: Angel, Nicola Zoe									
APPLICANT: Cooper, Benjamin Jay									
APPLICANT: Hart, Derek Nigel John									
TITLE OF INVENTION: Novel Polynucleotides and uses therefor									
FILE REFERENCE: 10338-180S									
CURRENT FILING DATE: 2004-06-24									
PRIOR APPLICATION NUMBER: PR9741/01									
PRIOR FILING DATE: 2001-12-24									
PRIOR APPLICATION NUMBER: PCT/AU02/01761									
PRIOR FILING DATE: 2002-12-24									
NUMBER OF SEQ ID NOS: 9									
SOFTWARE: PatentIn version 3.2									
SEQ ID NO 2									
LENGTH: 530									
TYPE: PRT									
ORGANISM: human									
US-10-876-285-2									
Query Match									
Best Local Similarity 100.0%; Score 2781; DB 5; Length 530;									
Best Local Similarity 100.0%; Pred. No. 1.5e-244;									
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	MSMDAMPLEPGVGBELKQAK	IEDAEKYSFMAVTYTKAPKKO	IOFADMQEFTKFTKTGR	60				
DB	1	MSMDAMPLEPGVGBELKQAK	IEDAEKYSFMAVTYTKAPKKO	IOFADMQEFTKFTKTGR	60				
QY	61	RSLSRSISQSTDSYSSAAS	YTDSDDEVSFPRKQOTNSKSS	NFCVNIQAEFGREI	120				
DB	61	RSLSRSISQSTDSYSSAAS	YTDSDDEVSFPRKQOTNSKSS	NFCVNIQAEFGREI	120				
QY	121	FIADQMSALISLKRKQGE	KPLAGAKIVGCTHTTAOTAV	ILETLCAAGACRWSACNY	180				
DB	121	FIADQMSALISLKRKQGE	KPLAGAKIVGCTHTTAOTAV	ILETLCAAGACRWSACNY	180				
QY	181	STONEVAALAEAGVAFAM	KGSEDDFWMCIDRCVNMDDG	QAMNILDGDLTHMYVKK	240				
DB	181	STONEVAALAEAGVAFAM	KGSEDDFWMCIDRCVNMDDG	QAMNILDGDLTHMYVKK	240				
QY	241	YPNVFKIRIGIVESVTG	VRHLYQLSFKAKLCVPA	NVNSVTYKQFDNLYCCRES	300				
DB	241	YPNVFKIRIGIVESVTG	VRHLYQLSFKAKLCVPA	NVNSVTYKQFDNLYCCRES	300				
QY	301	LKRITDVMFGKQVYVCG	YGVGKGCALKALGAIY	ITIEDICALQACMDGRVVKL	360				

Db 301 LKRTDVMFGKQVAVCGYEVGKGCALAKALGAIIVYTEIDPICALQACMDGFRVVKL 360
Qy 361 NEVIRQVDVITCTGNKNVVTREHLDKRNKSCIVCMGHSNTEIDVTSLRPELTWERVR 420
Db 361 NEVIRQVDVITCTGNKNVVTREHLDKRNKSCIVCMGHSNTEIDVTSLRPELTWERVR 420
Qy 421 SQVDHVIWPDGRVVLAEGRLLNLSCTVPTFVLSTATTQALALIELYNABEGRYKOD 480
Db 421 SQVDHVIWPDGRVVLAEGRLLNLSCTVPTFVLSTATTQALALIELYNABEGRYKOD 480
Qy 481 VYLLPKRMDDEVASLHLPSPDAHLTELTDQAKYLGKNGKPFKNYRY 530
Db 481 VYLLPKRMDDEVASLHLPSPDAHLTELTDQAKYLGKNGKPFKNYRY 530

RESULT 2
US-10-876-285-4
; Sequence 4, Application US/10876285
; Publication No. US20050044582A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Human
US-10-876-285-4

Query Match 100.0%; Score 2781; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.5e-244;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSMPAMPPLPGVGEELKQAKETIEDAKISFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
Db 1 MSMPAMPPLPGVGEELKQAKETIEDAKISFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
Qy 61 RLSLSISQSSSTDSYSSAASYTSSDDEVSPEKQOTNSKSSNFCVKNIKQAEFGRRRI 120
Db 61 RLSLSISQSSSTDSYSSAASYTSSDDEVSPEKQOTNSKSSNFCVKNIKQAEFGRRRI 120
Qy 121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAIVLETLICALGAOCRWASACNII 180
Db 121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAIVLETLICALGAOCRWASACNII 180
Qy 121 STONEVAALAAAGAVAFPAWKGESEDDFWWCIDRCVNDGQWANNILDDGGDLTHWVYK 240
Db 121 STONEVAALAAAGAVAFPAWKGESEDDFWWCIDRCVNDGQWANNILDDGGDLTHWVYK 240
Qy 181 STONEVAALAAAGAVAFPAWKGESEDDFWWCIDRCVNDGQWANNILDDGGDLTHWVYK 240
Db 181 STONEVAALAAAGAVAFPAWKGESEDDFWWCIDRCVNDGQWANNILDDGGDLTHWVYK 240
Qy 241 YPNVFKKIRGIIEBSVTGVHRLYQLSKAGKLCVPANVNDSVTKQFBNLYCCRESILDG 300
Db 241 YPNVFKKIRGIIEBSVTGVHRLYQLSKAGKLCVPANVNDSVTKQFBNLYCCRESILDG 300
Qy 301 LKRTDVMFGKQVAVCGYEVGKGCALAKALGAIIVYTEIDPICALQACMDGFRVVKL 360
Db 301 LKRTDVMFGKQVAVCGYEVGKGCALAKALGAIIVYTEIDPICALQACMDGFRVVKL 360
Qy 361 NEVIRQVDVITCTGNKNVVTREHLDKRNKSCIVCMGHSNTEIDVTSLRPELTWERVR 420
Db 361 NEVIRQVDVITCTGNKNVVTREHLDKRNKSCIVCMGHSNTEIDVTSLRPELTWERVR 420

Qy 421 SQVDHVIWPDGRVVLAEGRLLNLSCTVPTFVLSTATTQALALIELYNABEGRYKOD 480
Db 421 SQVDHVIWPDGRVVLAEGRLLNLSCTVPTFVLSTATTQALALIELYNABEGRYKOD 480
Qy 481 VYLLPKRMDDEVASLHLPSPDAHLTELTDQAKYLGKNGKPFKNYRY 530
Db 481 VYLLPKRMDDEVASLHLPSPDAHLTELTDQAKYLGKNGKPFKNYRY 530

RESULT 3
US-10-876-285-6
; Sequence 6, Application US/10876285
; Publication No. US20050044582A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
US-10-876-285-6

Query Match 100.0%; Score 2781; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.5e-244;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSMPAMPPLPGVGEELKQAKETIEDAKISFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
Db 1 MSMPAMPPLPGVGEELKQAKETIEDAKISFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
Qy 61 RLSLSISQSSSTDSYSSAASYTSSDDEVSPEKQOTNSKSSNFCVKNIKQAEFGRRRI 120
Db 61 RLSLSISQSSSTDSYSSAASYTSSDDEVSPEKQOTNSKSSNFCVKNIKQAEFGRRRI 120
Qy 121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAIVLETLICALGAOCRWASACNII 180
Db 121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAIVLETLICALGAOCRWASACNII 180
Qy 181 STONEVAALAAAGAVAFPAWKGESEDDFWWCIDRCVNDGQWANNILDDGGDLTHWVYK 240
Db 181 STONEVAALAAAGAVAFPAWKGESEDDFWWCIDRCVNDGQWANNILDDGGDLTHWVYK 240
Qy 241 YPNVFKKIRGIIEBSVTGVHRLYQLSKAGKLCVPANVNDSVTKQFBNLYCCRESILDG 300
Db 241 YPNVFKKIRGIIEBSVTGVHRLYQLSKAGKLCVPANVNDSVTKQFBNLYCCRESILDG 300
Qy 301 LKRTDVMFGKQVAVCGYEVGKGCALAKALGAIIVYTEIDPICALQACMDGFRVVKL 360
Db 301 LKRTDVMFGKQVAVCGYEVGKGCALAKALGAIIVYTEIDPICALQACMDGFRVVKL 360
Qy 361 NEVIRQVDVITCTGNKNVVTREHLDKRNKSCIVCMGHSNTEIDVTSLRPELTWERVR 420
Db 361 NEVIRQVDVITCTGNKNVVTREHLDKRNKSCIVCMGHSNTEIDVTSLRPELTWERVR 420
Qy 421 SQVDHVIWPDGRVVLAEGRLLNLSCTVPTFVLSTATTQALALIELYNABEGRYKOD 480
Db 421 SQVDHVIWPDGRVVLAEGRLLNLSCTVPTFVLSTATTQALALIELYNABEGRYKOD 480
Qy 481 VYLLPKRMDDEVASLHLPSPDAHLTELTDQAKYLGKNGKPFKNYRY 530
Db 481 VYLLPKRMDDEVASLHLPSPDAHLTELTDQAKYLGKNGKPFKNYRY 530

RESULT 4
US-10-683-610-1
; Sequence 1, Application US/10683610
; Publication No. US20050181450A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; TITLE OF INVENTION: A novel inositol 1,4,5-trisphosphate (IP3) receptor binding prote
; TITLE OF INVENTION: IP3
; FILE REFERENCE: PH-1852
; CURRENT APPLICATION NUMBER: US/10/683,610
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: JP 2002-299429
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-683-610-1

Query Match 100.0%; Score 2781; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1,5e-244;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSMPDAMPLPGVGBELKQAKETEDAEKYSFMAVTYTKAPKKQIOFADDMQEFTRPPTKTR	60
DB	1	MSMPDAMPLPGVGBELKQAKETEDAEKYSFMAVTYTKAPKKQIOFADDMQEFTRPPTKTR	60
QY	61	RLSRISISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVXNIKQAEFGREI	120
DB	61	RLSRISISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVXNIKQAEFGREI	120
QY	121	EIAEODMSALISLRRAOGEKPLAGAKIVGCTHITTAQTAVLLETICALGAOCRWSACNTY	180
DB	121	EIAEODMSALISLRRAOGEKPLAGAKIVGCTHITTAQTAVLLETICALGAOCRWSACNTY	180
QY	181	STONEVAALAEAGAVAFAMKGESEDDFMWCIDRCVNDGMOANMILDDGDLTHVYVK	240
DB	181	STONEVAALAEAGAVAFAMKGESEDDFMWCIDRCVNDGMOANMILDDGDLTHVYVK	240
QY	241	YPNVFKIRIGIYESVTGVHRLYQLSKAGKLCVPANVNDVTKQKFDNLCCRESILDG	300
DB	241	YPNVFKIRIGIYESVTGVHRLYQLSKAGKLCVPANVNDVTKQKFDNLCCRESILDG	300
QY	301	LKRTDVMFGGQVAVCGYGVGKCCALKALGAIYITTEIDPICALQACMDGFRVVKL	360
DB	301	LKRTDVMFGGQVAVCGYGVGKCCALKALGAIYITTEIDPICALQACMDGFRVVKL	360
QY	361	NEVIRQVAVITCTGNKQVITREHLDPMKNSCIVCMGHSNTEIDVTSIRTELTERVR	420
DB	361	NEVIRQVAVITCTGNKQVITREHLDPMKNSCIVCMGHSNTEIDVTSIRTELTERVR	420
QY	421	SCVDHVIWPDGKRVVLLAEGRLNLSCSTVPFVLSTATTOALALIELYNAPEGRYKOD	480
DB	421	SCVDHVIWPDGKRVVLLAEGRLNLSCSTVPFVLSTATTOALALIELYNAPEGRYKOD	480
QY	481	VYLLPKRNDYVASLHPSFDAHTELTDQAKYGLGNKGPFKPYRYX	530
DB	481	VYLLPKRNDYVASLHPSFDAHTELTDQAKYGLGNKGPFKPYRYX	530

RESULT 5
US-09-782-051-2
; Sequence 2, Application US/09782051
; Patent No. US20020035078A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
; TITLE OF INVENTION: (AHcy) type activity

FILE REFERENCE: 24305 MRB
; CURRENT APPLICATION NUMBER: US/09/782,051
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: PCT/NZ97/00133
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: NZ 299507
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-051-2

Query Match 100.0%; Score 2781; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 1,9e-244;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSMPDAMPLPGVGBELKQAKETEDAEKYSFMAVTYTKAPKKQIOFADDMQEFTRPPTKTR	60
DB	85	MSMPDAMPLPGVGBELKQAKETEDAEKYSFMAVTYTKAPKKQIOFADDMQEFTRPPTKTR	144
QY	61	RLSRISISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVXNIKQAEFGREI	120
DB	145	RLSRISISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVXNIKQAEFGREI	204
QY	121	EIAEODMSALISLRRAOGEKPLAGAKIVGCTHITTAQTAVLLETICALGAOCRWSACNTY	180
DB	205	EIAEODMSALISLRRAOGEKPLAGAKIVGCTHITTAQTAVLLETICALGAOCRWSACNTY	264
QY	181	STONEVAALAEAGAVAFAMKGESEDDFMWCIDRCVNDGMOANMILDDGDLTHVYVK	240
DB	265	STONEVAALAEAGAVAFAMKGESEDDFMWCIDRCVNDGMOANMILDDGDLTHVYVK	324
QY	241	YPNVFKIRIGIYESVTGVHRLYQLSKAGKLCVPANVNDVTKQKFDNLCCRESILDG	300
DB	325	YPNVFKIRIGIYESVTGVHRLYQLSKAGKLCVPANVNDVTKQKFDNLCCRESILDG	384
QY	301	LKRTDVMFGGQVAVCGYGVGKCCALKALGAIYITTEIDPICALQACMDGFRVVKL	360
DB	385	LKRTDVMFGGQVAVCGYGVGKCCALKALGAIYITTEIDPICALQACMDGFRVVKL	444
QY	361	NEVIRQVAVITCTGNKQVITREHLDPMKNSCIVCMGHSNTEIDVTSIRTELTERVR	420
DB	445	NEVIRQVAVITCTGNKQVITREHLDPMKNSCIVCMGHSNTEIDVTSIRTELTERVR	504
QY	421	SCVDHVIWPDGKRVVLLAEGRLNLSCSTVPFVLSTATTOALALIELYNAPEGRYKOD	480
DB	505	SCVDHVIWPDGKRVVLLAEGRLNLSCSTVPFVLSTATTOALALIELYNAPEGRYKOD	564
QY	481	VYLLPKRNDYVASLHPSFDAHTELTDQAKYGLGNKGPFKPYRYX	530
DB	565	VYLLPKRNDYVASLHPSFDAHTELTDQAKYGLGNKGPFKPYRYX	614

RESULT 6
US-11-110-748-2
; Sequence 2, Application US/11110748
; Publication No. US20050282765A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
; TITLE OF INVENTION: (AHcy) type activity
; FILE REFERENCE: 24305 MRB
; CURRENT APPLICATION NUMBER: US/11/110,748
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: PCT/NZ97/00133
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: NZ 299507
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2
LENGTH: 614
TYPE: prt
ORGANISM: Homo sapiens
US-11-110-748-2

Query Match 100.0%; Score 2781; DB 6; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.9e-244;
Matches 530; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSMPDMPPLPGGEELKQAEIEDAEKYSFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
85 MSMPDMPPLPGGEELKQAEIEDAEKYSFMAVTYTKAPKKQIOFADDMQEFKPTKTR 144
61 RLSRSISQSSSTDYSSAASYTDSDDDEVS PREKQOTNSKSSNFCVKNIKOAEFGREI 120
145 RLSRSISQSSSTDYSSAASYTDSDDDEVS PREKQOTNSKSSNFCVKNIKOAEFGREI 204
121 EIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAQTAVLLETICALGACRMSACNLY 180
205 EIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAQTAVLLETICALGACRMSACNLY 264
181 STONEVAALAEAGAVAFAMKGESEDDFWMCIDRCVNMDCMOANMILDDGGDLTHVYKK 240
265 STONEVAALAEAGAVAFAMKGESEDDFWMCIDRCVNMDCMOANMILDDGGDLTHVYKK 324
241 YNNVEFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVNDVTKQFDMLYCCRESILDG 300
345 YNNVEFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVNDVTKQFDMLYCCRESILDG 384
301 LKRTDWMFGKQVAVCGEYVGGCCALKALGAIYITEIDPICALQACMDGFRVVL 360
385 LKRTDWMFGKQVAVCGEYVGGCCALKALGAIYITEIDPICALQACMDGFRVVL 444
361 NEVIRQVDVITCTGNKVVYTRHLD RMKNSCIVCMGHSNTEIDVTSIRTELTWERV 420
445 NEVIRQVDVITCTGNKVVYTRHLD RMKNSCIVCMGHSNTEIDVTSIRTELTWERV 504
421 SQVDHVIMPDGKRVVLLAEGRLNLSCTVPFVLSITATTOALALIELYNAPGRYKOD 480
505 SQVDHVIMPDGKRVVLLAEGRLNLSCTVPFVLSITATTOALALIELYNAPGRYKOD 564
481 VYLLPRKMDDEVYASLHLPFDALHTELTDQAKYIGLNKNGPFKNYYRY 530
565 VYLLPRKMDDEVYASLHLPFDALHTELTDQAKYIGLNKNGPFKNYYRY 614

RESULT 7
US-10-876-285-8

Sequence 8, Application US/10876285
Publication No. US20050044582A1
GENERAL INFORMATION:
APPLICANT: Kato, Masato
APPLICANT: Angel, Nicola Zoe
APPLICANT: Cooper, Benjamin John
APPLICANT: Hart, Derek Nigel Jay
TITLE OF INVENTION: Novel Polynucleotides and uses therefor
FILE REFERENCE: 10338-18US
CURRENT APPLICATION NUMBER: US/10/876,285
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: PR9741/01
PRIOR FILING DATE: 2001-12-24
PRIOR APPLICATION NUMBER: PCT/AU02/01761
PRIOR FILING DATE: 2002-12-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 530
TYPE: prt
ORGANISM: Mouse
US-10-876-285-8

Query Match 99.9%; Score 2778; DB 5; Length 530;

Best Local Similarity 99.8%; Pred. No. 2.8e-244;
Matches 529; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

1 MSMPDMPPLPGGEELKQAEIEDAEKYSFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
1 MSMPDMPPLPGGEELKQAEIEDAEKYSFMAVTYTKAPKKQIOFADDMQEFKPTKTR 60
61 RLSRSISQSSSTDYSSAASYTDSDDDEVS PREKQOTNSKSSNFCVKNIKOAEFGREI 120
61 RLSRSISQSSSTDYSSAASYTDSDDDEVS PREKQOTNSKSSNFCVKNIKOAEFGREI 120
121 EIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAQTAVLLETICALGACRMSACNLY 180
121 EIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAQTAVLLETICALGACRMSACNLY 180
181 STONEVAALAEAGAVAFAMKGESEDDFWMCIDRCVNMDCMOANMILDDGGDLTHVYKK 240
181 STONEVAALAEAGAVAFAMKGESEDDFWMCIDRCVNMDCMOANMILDDGGDLTHVYKK 240
241 YNNVEFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVNDVTKQFDMLYCCRESILDG 300
241 YNNVEFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVNDVTKQFDMLYCCRESILDG 300
301 LKRTDWMFGKQVAVCGEYVGGCCALKALGAIYITEIDPICALQACMDGFRVVL 360
301 LKRTDWMFGKQVAVCGEYVGGCCALKALGAIYITEIDPICALQACMDGFRVVL 360
361 NEVIRQVDVITCTGNKVVYTRHLD RMKNSCIVCMGHSNTEIDVTSIRTELTWERV 420
361 NEVIRQVDVITCTGNKVVYTRHLD RMKNSCIVCMGHSNTEIDVTSIRTELTWERV 420
421 SQVDHVIMPDGKRVVLLAEGRLNLSCTVPFVLSITATTOALALIELYNAPGRYKOD 480
421 SQVDHVIMPDGKRVVLLAEGRLNLSCTVPFVLSITATTOALALIELYNAPGRYKOD 480
481 VYLLPRKMDDEVYASLHLPFDALHTELTDQAKYIGLNKNGPFKNYYRY 530
481 VYLLPRKMDDEVYASLHLPFDALHTELTDQAKYIGLNKNGPFKNYYRY 530

RESULT 8
US-10-756-149-5569

Sequence 5569, Application US/10756149
Publication No. US20050181375A1
GENERAL INFORMATION:
APPLICANT: Azic, Natasha
APPLICANT: Zlotnick, Albert
TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
FILE REFERENCE: file
CURRENT APPLICATION NUMBER: US/10/756,149
CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5569
LENGTH: 619
TYPE: prt
ORGANISM: Homo Sapiens
US-10-756-149-5569

Query Match 88.1%; Score 2449.5; DB 5; Length 619;
Best Local Similarity 84.7%; Pred. No. 3.5e-214;
Matches 466; Conservative 33; Mismatches 24; Indels 27; Gaps 3;

8 PLPGVGE-----ELKQAEIEDAEKYSFMAVTYTKAPK--K 40
70 PVPDGGSGPAAALSPAAGKVPQASAMKRSDPHQHQRHDDGGEALVSPDGTVEAPRTVK 129
41 QIOFADDMQEFKPTKGRSLRSISQSSSTDYSSAASYTDSDDDEVS PREKQOTNSK 100
130 KIQADQKQEFKRTKIGRSLRSISQSSSTDYSSAASYTDSDDDEVS PREKQOTNSK 189
101 GSNFCVKNIKOAEFGREIEIAEODMSALSLRRAQGEKPLAGAKIVGCTHTTAQTAV 160

```

Db 190 GSSDFCVKNIQAFGRREIEIAEQEMPALMLAKRRAPAGEKPLAGAKIVGCTHTTAQTAIV 249
Qy 161 LIETLCALGAQCRWSACNIYSTONEVAAALAEAGVAVPAMKGESEDDPFWMCIDRCVNMDD 220
Db 250 LMETLGAQACRMAACNIYSTLNEVAAALAEAGSPVAVPAMKGESEDDPFWMCIDRCVNEG 309
Qy 221 WQANMILDDGDLTHWYKYPNVFKIRGIVEBSVTGVRLYOLSKAKGLCPVAMVND 280
Db 310 WQPMILDDGDLTHWYKYPNVFKIRGIVEBSVTGVRLYOLSKAKGLCPVAMVND 369
Qy 281 SVTQKQEDNLCCRESILDKKRTTDVWFGKQVYVCGYGVGCCALALGATVIT 340
Db 370 SVTQKQEDNLCCRESILDKKRTTDVWFGKQVYVCGYGVGCCALALGATVIT 429
Qy 341 EIDPICALQACMDGFRVLKNEVIRQVDVITCTGNKVVVREHLDRKNSCIVCMGHS 400
Db 430 EIDPICALQACMDGFRVLKNEVIRQVDVITCTGNKVVVREHLDRKNSCIVCMGHS 489
Qy 401 NTEIDVTSLRPELTWERVRSQVDHVIVPDGRVLLAEGRLNLSCSTVPFVLSTAT 460
Db 490 NTEIDVTSLRPELTWERVRSQVDHVIVPDGRVLLAEGRLNLSCSTVPFVLSTAT 549
Qy 461 TQALALIELVNAPEGRYKQDYLPLPKMDEVYASLHPSFDAHLTELDDQAKYLGLNKN 520
Db 550 TQALALIELVNAPEGRYKQDYLPLPKMDEVYASLHPSFDAHLTELDDQAKYLGLNKN 609
Qy 521 GPFKNRYRY 530
Db 610 GPFKNRYRY 619

```

```

PRIORITY APPLICATION NUMBER: US 60/278,480
PRIOR FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: US 60/278,479
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 564
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No: 7484737CD1
US-10-467-903-1
Query Match 87.3%; Score 2429; DB 5; Length 564;
Best Local Similarity 90.3%; Pred. No. 2,36-212;
Matches 455; Conservative 24; Mismatches 25; Indels 0; Gaps 0;

```

```

RESULT 9
US-10-467-903-1
Sequence 1, Application US/10467903
Publication No. US20040265807A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION
APPLICANT: SANJANA, Madhusudan M.
APPLICANT: LU, Yan
APPLICANT: LEE, Ernestine A.
APPLICANT: HAFALIA, April J.A.
APPLICANT: WARREN, Bridget A.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: YAO, Monique G.
APPLICANT: LEE, Sally
APPLICANT: THORNTON, Michael B.
APPLICANT: CHAWLA, Nandinder K.
APPLICANT: XU, Yuning
APPLICANT: TRAN, Yuen K.
APPLICANT: LAU, Preeti G.
APPLICANT: LU, Dyang, Anita M.
APPLICANT: SWARNAKAR, Anita
APPLICANT: RING, Huijun Z.
APPLICANT: JONES, Karen A.
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: PI-0360 USN
CURRENT APPLICATION NUMBER: US/10/467,903
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/US02/03814
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/268,113
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/269,215
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/272,271
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US 60/274,091
PRIOR FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/274,423
PRIOR FILING DATE: 2001-03-09

```

```

RESULT 10
US-11-097-143-2781
Sequence 2781, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
APPLICANT: Ventier, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19

```



```

QY      164 TLCAAGACRMASACNIYSTONEVAALAAAGVAVFAMKGESEDDFWMCIDRCVNM-DGMQ 222
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61 TLTAAGADVRMASCNIFSTQDHAAAIAKAGTVPFAFKGESLDEYWFESHRIPEWPNGEF 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      223 ANMIILDDGGDLTHM-----VYKK-----YRNVFKK 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      121 ANMIILDDGGDALTLILLGSKAEKDRSVISKPTNEEVALYKSIERHLADPTWYSTRLAH 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      248 IRGIVEESVTGVHRLYQLSKAGKLCVPAWNVDSVTKOKFBNLYCCRESILDLGKRTTQV 307
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      181 IKGVTBETTTGVHRLYQMEKEGRLPPFALINVDSVTKSKFDNLXGRESLVDGICRATDV 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      308 MFGKQVNVCGYGEVKGCCCAALKALGAIYVITEIDPICALQACMDGFRVVKLNEVIRQV 367
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      241 MIAGKIADVAGYGVKGCAQSLRGIGATVWTEIDPICALQAMEGVRVVTMEYAADKA 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      366 DVVITCTGNKVVNTEHLDKRNKSCICVCMGHSNTEIDVTSLRTELPETMERVSQVDHYI 427
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      301 DLFVATGNYHYIGHDHMKAMRHNAICNIGHFDSRIDVASTR--OYQMDNIKPOVDHII 358
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      428 WPDGKRVVLLAEGRLNLSGST-VPTFVLSITATTOALALIELYNAPBGRYKQDVYLLPK 486
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      359 FPDGKRVVLLAEGRLVNLGATGHPSEFVMSNFTQTQIAQIELF--TQGNKYENKYYVLPK 417
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      487 KNDVEYASLHLPSPDAHLTELTDQAKYLGLKNKNGPFKNYRY 530
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      418 HIDEKVARLHLARIGANLTVLSDEQAGYIGVDKNGPFKNHYRY 461
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

RESULT 15

```

US-10-369-493-7543
/ Sequence 7543, Application US/10369493
/ Publication No. US20030233675A1
/ GENERAL INFORMATION:
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Cao, Yongwei
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Chen, Xianfeng
/ TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
/ FILE REFERENCE: 38-10(52052)B
/ CURRENT APPLICATION NUMBER: US/10/369,493
/ PRIOR FILING DATE: 2003-02-28
/ PRIOR APPLICATION NUMBER: US 60/360,039
/ NUMBER OF SEQ ID NOS: 47374
/ SEQ ID NO 7543
/ LENGTH: 461
/ TYPE: PRT
/ ORGANISM: Burkholderia cepacia
US-10-369-493-7543

```

```

Query Match      42.7%; Score 1187; DB 4; Length 461;
Best Local Similarity 50.4%; Pred.No.4.3e-99;
Matches 234; Conservative 80; Mismatches 110; Indels 40; Gaps 6;

```

```

QY      104 NFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHITAQTAVLIE 163
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      1 DFIIVADMSLADWGRKELNIAETEMPGVQFREYKVVQPLKGRARINGSLSLHMTIQTVLIE 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      164 TLCAAGACRMASACNIYSTONEVAALAAAGVAVFAMKGESEDDFWMCIDRCVNM-DGMQ 222
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      61 TLTAAGADVRMASCNIFSTQDHAAAIAKAGTVPFAFKGESLDEYWFESHRIPEWPNGEF 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      223 ANMIILDDGGDLTHM-----VYKK-----YRNVFKK 247
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      121 ANMIILDDGGDALTLILLGSKAEKDRSVISKPTNEEVALYKSIERHLADPTWYSTRLAH 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      248 IRGIVEESVTGVHRLYQLSKAGKLCVPAWNVDSVTKOKFBNLYCCRESILDLGKRTTQV 307
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      181 IKGVTBETTTGVHRLYQMEKEGRLPPFALINVDSVTKSKFDNLXGRESLVDGICRATDV 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

QY      308 MFGKQVNVCGYGEVKGCCCAALKALGAIYVITEIDPICALQACMDGFRVVKLNEVIRQV 367
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      241 MIAGKIADVAGYGVKGCAQSLRGIGATVWTEIDPICALQAMEGVRVVTMEYAADKA 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      366 DVVITCTGNKVVNTEHLDKRNKSCICVCMGHSNTEIDVTSLRTELPETMERVSQVDHYI 427
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      301 DLFVATGNYHYIGHDHMKAMRHNAICNIGHFDSRIDVASTR--OYQMDNIKPOVDHII 358
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      428 WPDGKRVVLLAEGRLNLSGST-VPTFVLSITATTOALALIELYNAPBGRYKQDVYLLPK 486
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      359 FPDGKRVVLLAEGRLVNLGATGHPSEFVMSNFTQTQIAQIELF--TQGNKYENKYYVLPK 417
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      487 KNDVEYASLHLPSPDAHLTELTDQAKYLGLKNKNGPFKNYRY 530
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
      418 HIDEKVARLHLARIGANLTVLSDEQAGYIGVDKNGPFKNHYRY 461
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Search completed: September 6, 2006, 19:57:40
Job time : 178.283 secs

```



```

QY 397 MGHSTNTEIDVTSRTELTWERVRSQVDHVPDGRVLLAEGRLNLSCS--TVPFVYL 455
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 300 IGHFDTEIGVAMKANAASVSEIKPOVHRYTMGNQNHVILLAEGRVLNIGCAHGPSFWM 359
QY 456 STATTQALALIELY--NAPEGRY----KODVYLLPKKMDYVASLHLPSEDAHLELTD 510
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 360 SNSFCNQVIAQLELMTNRITTDKYPGPOKDVFFIPKLEDEKVAALHGLKGLAKTLKLTPE 419
QY 511 QAKYLGLNKGPKPKMYRY 530
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 420 QADYINVSAGPFPKPSHYR 439

RESULT 2
US-10-449-902-43217
; Sequence 43217, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 43217
; LENGTH: 485
; TYPE: PRF
; ORGANISM: Oryza sativa
US-10-449-902-43217

Query Match          39.9%; Score 1110; DB 6; Length 485;
Best Local Similarity 45.4%; Pred. No. 2.7e-80;
Matches 219; Conservative 91; Mismatches 124; Indels 48; Gaps 7;

QY 95 QQTNSGSSNFCVKNIKQAEFGREIEIAEODMSALISLRKAQGEKPLAGAKIVCTTH 154
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 6 EKTSS--GREYKXKDSQADFGRLEIEAEVEMPGMACRAEPGPOPFGARISGSLHM 63
QY 155 TQOTAVLITLCAQOCRSACNIYSTONEVAALAEAGVANPAFKGSEDDFMFCIR 214
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 TQOTAVLITLCAQOCRSACNIYSTONEVAALAEAGVANPAFKGSEDDFMFCIR 123
QY 215 CVMMD-GMOAMMILDDGDLTHWYK----- 239
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 CIDMGVGGGPDILVDDGGATLLIHGVAEEFEKSGKVPDESTDNAEFKVLITIRD 183
QY 240 -----KTPNFKTRIGYVESVTGVHRLYQLSKQKGLCVPMANNVDSYTKKPFNLIC 292
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 GKSDPSKTRKMERLVGVSEETTTGVKRLYQOETGALLFPFINVNDVYTKSPFNLVG 243
QY 293 CRESIDLGKRTDWMFEGKQVAVCGYEGKGCCKALKALGAIYITTEIDPICALQACQ 352
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 244 CRHSLPDGLMRATDVMAGVAVACGIDVGKCAALAKGARKVYVTEIDPICALQALM 303
QY 353 DGFRRVYKLEVIRQVDVITCTGNKRVVTRHLDKMKNSCIVCMGHSTNTEIDVTSLRT- 411
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 304 EGIQVLTLEDDVSEADIPVTTGNKDIIMVDHMKKKNNAIVCNIGHFDEIDMLGLETY 363
QY 412 PELTMRVNSQVDHVPD--GKRVVLLAEGRLNLSCS--TVPFVYSTATTQALALIEL 469
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 364 PGVKRITIKQIDRWVFPETNTGIVLAEGRLNLGATGHPFVWSCFTQNVIAQLEI 423
QY 470 YNAPF--GRYKQDYYLLPKKMDYVASLHLPSEDAHLELTDPAKTLGKLNKGPFPKMY 528
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

Db 424 WEKSTGYEKKVYVLPRLHDEKVAALHGLKGLARLTLSKSQADYISVPEEGPYKPAHY 483
QY 529 RY 530
  ||
Db 484 RY 485

RESULT 3
US-10-953-349-5927
; Sequence 5927, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 5927
; LENGTH: 291
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5927

Query Match          27.8%; Score 773; DB 6; Length 291;
Best Local Similarity 50.9%; Pred. No. 8.6e-54;
Matches 147; Conservative 60; Mismatches 78; Indels 4; Gaps 4;

QY 246 KIRIRIVESVTVGRRLYQLSKQKGLCVPMANNVDSYTKKPFNLICCRESTIDGKRTT 305
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ERLVGVSEETTTGVKRLYQOQNGTLLFPALVNDVYTKSPFNLICRHSLPDGLMRAT 62
QY 306 DVMFGKQVAVCGYEGKGCCKALKALGAIYITTEIDPICALQACMDGFRVYKLVNVR 365
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 DVMINGKVAVIGCYDVGKCAAMKTAGARIYVTEIDPICALQALMGLOVLTLEDVVS 122
QY 366 QVDVAVITCTGNKRVVTRHLDKMKNSCIVCMGHSTNTEIDVTSLRT--BELTMRVRSQVD 424
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 EADIVTTTGNMDIIMVDMRMRKNNNAIVCNIGHFDEIDMLGLETYGVKRIITKPTD 182
QY 425 HYIWDGR--VLLAEGRLNLSCS--TVPFVYSTATTQALALIELVN--APEGRYKQDV 481
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 RNVFPETAGIIVLAEGRLLNLGCAITGHPFVWSCFTQNVIAQLELNMKASGITEKYV 242
QY 482 YLLPKKMDYVASLHLPSEDAHLELTDPAKTLGKLNKGPFPKMYRY 530
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 243 YLLPRLHDEKVAALHGLKGLARLTLSKSDQSDYVSIPIEGFPKPPHYR 291

RESULT 4
US-10-953-349-5928
; Sequence 5928, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patent In version 3.3
; SEQ ID NO 5928
; LENGTH: 270
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5928

Query Match          25.8%; Score 718; DB 6; Length 270;
Best Local Similarity 50.7%; Pred. No. 1.8e-49;
Matches 137; Conservative 55; Mismatches 74; Indels 4; Gaps 4;

```

QY 265 LSKAGKLCVPMANNVDSYTKOKFDNLCCRESILDLKRTTDMFGKOVVCGYGEVXK 324
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 1 MOQNSTLFPALNVDSYTKSKFDNLCCRESILDLKRTTDMFGKOVVCGYGEVXK 60
 QY 325 GCCAALKALGAIYVITEIDPICALQACMDGFRVVKLINEVIRQDVVITCTGNKKNVTRRH 384
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 61 GCAAMKTAGARAVITEIDPICALQALMEGLQVLTLEDVVSADIFVTTGNKDIIMVDH 120
 QY 385 LDRMKNKSCIVCMGHSNTEIDVTSIRT-PELTWERVRSQVDVIMPDGKR-VLLAEGRL 442
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 121 MKMKNNAIIVCNIGHFDEIDMLGLETYPGVKRIITKPTDWMVPEPKAGIIVLAEGRL 180
 QY 443 LNLSCST-VPTFVLSTATTQALALIELYN-APEGRKQDVYLLPKKQDEYVASLHLPST 500
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 181 MNLGATGHPSPVMSCSFTNQVIAOLELWNEKASGKTEKAVYVLRKHDEKVALHLGL 240
 QY 501 DAHLTELTDQAKYGLGNKNGPFPKNYRY 530
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 241 GARLTKLSKQSDVYSIPIEGPYKPPHYRY 270

RESULT 5

US-10-449-902-30161
 ; Sequence 30161, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A02051-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; PRIORITY FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIORITY FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30161
 ; LENGTH: 270
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-30161

Query Match 25.6%; Score 711; DB 6; Length 270;
 Best Local Similarity 50.4%; Pred. No. 6-6e-49;
 Matches 136; Conservative 54; Mismatches 76; Indels 4; Gaps 4;

QY 265 LSKAGKLCVPMANNVDSYTKOKFDNLCCRESILDLKRTTDMFGKOVVCGYGEVXK 324
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 1 MOQNSTLFPALNVDSYTKSKFDNLCCRESILDLKRTTDMFGKOVVCGYGEVXK 60
 QY 325 GCCAALKALGAIYVITEIDPICALQACMDGFRVVKLINEVIRQDVVITCTGNKKNVTRRH 384
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 61 GCAAMKTAGARAVITEIDPICALQALMEGLQVLTLEDVVSADIFVTTGNKDIIMVDH 120
 QY 385 LDRMKNKSCIVCMGHSNTEIDVTSIRT-PELTWERVRSQVDVIMPDGKR-VLLAEGRL 442
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 121 MKMKNNAIIVCNIGHFDEIDMLGLETYPGVKRIITKPTDWMVPEPKAGIIVLAEGRL 180
 QY 443 LNLSCST-VPTFVLSTATTQALALIELYN-APEGRKQDVYLLPKKQDEYVASLHLPST 500
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 181 MNLGATGHPSPVMSCSFTNQVIAOLELWNEKASGKTEKAVYVLRKHDEKVALHLGL 240
 QY 501 DAHLTELTDQAKYGLGNKNGPFPKNYRY 530
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 241 GARLTKLSKQSDVYSIPIEGPYKPPHYRY 270

RESULT 6

US-10-953-349-5929
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929

Query Match 21.4%; Score 595; DB 6; Length 233;
 Best Local Similarity 48.7%; Pred. No. 9.1e-40;
 Matches 113; Conservative 51; Mismatches 64; Indels 4; Gaps 4;

QY 303 RTDVMFGKOVVCGYGEVXKCCALKALGAIYVITEIDPICALQACMDGFRVVKLINE 362
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 2 RATDVMTAGKVAVIGYGVGKCAAMKTAGARAVITEIDPICALQALMEGLQVLTLED 61
 QY 363 VIRQDVVITCTGNKKNVTRRHLDPMKNSCIVCMGHSNTEIDVTSIRT-PELTWERVRS 421
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 62 VVSADIFVTTGNKDIIMVDHMKMKNNAIIVCNIGHFDEIDMLGLETYPGVKRIITKP 121
 QY 422 QVDVIMPDGKR-VLLAEGRLNLSCST-VPTFVLSTATTQALALIELYN-APEGRYK 478
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 122 QTDWVPEPKAGIIVLAEGRLMNLGATGHPSPVMSCSFTNQVIAOLELWNEKASGKTE 181
 QY 479 QDVYLLPKKQDEYVASLHLPSTDAHLTELTDQAKYGLGNKNGPFPKNYRY 530
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 182 KKVYVLRKHDEKVALHLGLGARTLTKSKQSDVYSIPIEGPYKPPHYRY 233

RESULT 7

US-10-449-902-30934
 ; Sequence 30934, Application US/10449902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A02051-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; PRIORITY FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIORITY FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 30934
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-30934

Query Match 21.1%; Score 587; DB 6; Length 233;
 Best Local Similarity 48.7%; Pred. No. 3.9e-39;
 Matches 113; Conservative 49; Mismatches 66; Indels 4; Gaps 4;

QY 303 RTDVMFGKOVVCGYGEVXKCCALKALGAIYVITEIDPICALQACMDGFRVVKLINE 362
 ; Sequence 5929, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579PUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; PRIORITY FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 5929
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; US-10-953-349-5929
 Db 2 RATDVMTAGKVAVIGYGVGKCAAMKTAGARAVITEIDPICALQALMEGLQVLTLED 61
 QY 363 VIRQDVVITCTGNKKNVTRRHLDPMKNSCIVCMGHSNTEIDVTSIRT-PELTWERVRS 421

```
Db 62 VVSADLVFTTGGKIDIMWDMKRNNAIVCNIHFDNEIDMLGETPGVKRITIK 121
Qy 422 QVDHVIMPD-GKRVLLAEGRLNLSCST-VPTFVLSTATTQALALIEYNAPG-GRYK 478
Db 122 QTRRWVFPENTTGIIVLAEGRLNLGCATGHPSTVMSCSFTNOVIAOLEMKESSTKYE 181
Qy 479 QDVYLLPKKDEYVASLHLPSEFPAHTELTDDQAKYLGKNGKPKPNYRY 530
Db 182 KKVYVLPKHLDKVAALHLKGLGRLTKLSKQADYISVPEGPKAHARY 233

RESULT 8
US-10-449-902-43902
; Sequence 43902, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43902
; LENGTH: 1129
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43902

Query Match
Best Local Similarity 4.1%; Score 113.5; DB 6; Length 1129;
Matches 94; Conservative 77; Mismatches 160; Indels 187; Gaps 24;

Qy 55 PRTGRRS-----LSRSISOSTD-----SYSSAASYDSSDDESPRE----- 93
Db 567 PSTYTKRNEVLNLOARHKSDBENLOERGMOHGLSNADNPDDHASSSAPVETDL 626
Qy 94 ----KOOTSKSSSNFCVKNIKQAEFGREIEIAEODMSALISLRKKAQGEKPLAOKIV 149
Db 627 VLCTPRDCSSKSSSTCSKVEDSE---RSVHLVPKKVDL-NLKHQQLSVCP----- 675
Qy 150 GCHITIAQTVLLETLCALGAOCRMSCNITSTONEVAAALAEAGVAFPA-WKGESEDDP 208
Db 676 -----NSCSWSSINVGKTSHTLSHVASGGSFAFQWQKRSP--- 712
Qy 209 WWCIDRCVNMDDQANNILDDGDLTHWVYKXYPNVFKIRGIYESVTGVRHLVQLSKA 268
Db 713 -----LAQNSDLN--YKLVERLFPKVGQBEAVSAICSIYRCRS 753
Qy 269 GK-----LCVPANVNDVTKQKF-----DNLYCCREST--LD-GLKRTDVMF 309
Db 754 TESRRGSRNDIWLQ---FHGSDSMAKRIYVALAEIMHGSKENLIYDLNLQMDSSSP 810
Qy 310 GGGQVAVVCGEYVGGKGCALKALGAVITTEIDPI-CAQAQCMDF-----RY 357
Db 811 RGTGTGIDCIVEOLS-----KRRRSVLFNDIDRADCLVQDSLPAIKSGFQDMRGKV 863
Qy 358 VKLNEVIRQVDVITCTGNKVVTRREHIDRMKNSCIQNGHSHTEIDVTSLTPELTWE 417
Db 864 VDLNDSI-----VLSRSMIHSGKNG---LEEGLSFSEKILATR----- 900
Qy 418 RVRSQVDHVIMPDKRVLLAE-GRLLNLSCTVPTFVLSTATTQALALIELYNAPG 476
Db 901 -----GHRLLIIVERGPAITSGC-----PSGK 922
```

```
Qy 477 YKODVYLLPKK-MDEVVASLHLPSEFPAHTELTDDQAK 513
Db 923 ----VVVSPRHFLTKIQASLCSGSSISKRLXMSDDQEK 956

RESULT 9
US-10-449-902-55937
; Sequence 55937, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agricultural Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 55937
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-55937

Query Match
Best Local Similarity 3.9%; Score 109; DB 6; Length 317;
Matches 52; Conservative 32; Mismatches 75; Indels 66; Gaps 8;

Qy 296 SILDLGKRTDVMFG-----GKQVAVVCGEYVGGKGCALKALGAVIYT 340
Db 37 NIFHGKRVVDLCAPGSMQVLSRNLVYPAKQSPDKCKGL-----PLIVAI 84
Qy 341 EIDPICALQACMDGRVYVKNLEVIROVDVITCTGNKVVTRREHIDRMKNSCIQNGHS 400
Db 85 DLQPMAPL-----EGVIOVGQDITNARTAEVIR-HFDGCRADLVVDCGAP- 129
Qy 401 NHEIDVTSLRTELTWERRSQ-----VDHVIMPDKRVLLAEGRLNLSCSTVPT 452
Db 130 ----DVTLHMD---EFVQSOLIIALTLITVHLVKGKVFYAKIFRGKOTSLLYCQLKL 182
Qy 453 FVLSTI-----ATTQALALIELYNAPGGRYKQDVYLLPKKM 488
Db 183 FFSQVTFAPKRSRNSISIAFAVCENISPPBGFKEKDLHYHLEKV 227

RESULT 10
US-11-056-355B-45994
; Sequence 45994, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brovet, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 45994
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: peptide
; LOCATION: (1)..(663)
```

OTHER INFORMATION: Ceres Seq. ID no. 12600203
US-11-056-355B-45994

Query Match	3.9%	Score 108;	DB 7;	Length 663;
Best Local Similarity	18.6%	Prod No. 3 2.		

```

QY      74 SYSAASTDSDDDEVSREKOOTSSKSSNFCVNIKOAEFGREIEIAEDMALLSI 133
Db      43 SCSAASGSHLRNLHRCRRRTNGNNNGVAQFVAGKKKEELANER---IKDEVLSTAVNV 99
QY      134 RKRAOGEK-----PLAGAKIVCGTHITATQAVALIET 164
Db      100 RYEHEKEHEHDENVNVSMGLDRCRFRDLARMILHGFLPSMEDVGFRFNIGLLOPFEEL 159
QY      165 LC--ALGAOCRWASACNIYSTQ--NEVNAAL---AEGAVALVFAMKESBEDDFWICIDRCVN 217
Db      160 VAFERVESDC---MEIYAKEKHKIPELDLDPKGISISVDVMSGSGSDDELCL----- 210
QY      218 MDGMQANNILDDGGDLTHVVYKKYPNVFKKIRGIYESVTGV-----HR 261
Db      211 ----AAHYIDEGBELK---KRVINPF---MYDPHSGEMLEAVIMTCLMEWDIDRK 256
QY      262 LYOLSKAGKLCPV-----AMRVNDSVTROKFPDNLYCCRESILDGLKRTTDVWFGGQYVV 316
Db      257 LF--SMAASHAPRPSENAVASKIRBLSONKF--LVC-----YGLFDVS 296
QY      317 CGYGEVG-----KGCCALKAL- GAIVYTEIDPICALOACMDGFVVKLVNEVIROYD 368
Db      297 CGVAVINEMVQDSLPCACDTINIIESIRYVKSESI-----ODRF-----NQMIIVEVG 345
QY      369 VV-----ITCTGNKNVYTRHEDLMKNSCIVCMGMSGNTEIDVTSIRT-P-E 413
Db      346 AVSERNLICIDDPKRWDSICTMLLENLAEOKSAFSLNW-----EHPDVSUVCSD 393
QY      414 LTMERVASQVDHAVIMPDGKRVLLAEGRLNLSCESTVEFTVLSITATTQATALIELYNAP 473
Db      394 LEWERLTGTIVFFL-----KVFEVINAFTKSSC--LPANMFPEVCDIHLLIEMSKNP 445
QY      474 EGRYKQDVYLLPKRMDEX-----VASLHLPEFDAHLTE 506
Db      446 DDFISSLVNMNRKFPDDWKQNYLVLAATTIDPFKKKLYE 487

```

```

RESULT 11
US-11-056-355B-45993
; Sequence 45993: Application US/11056355B
; Publication NO: US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence determined DNA fragments and corresponding
; TITLE OF INVENTION: Polypeptides encoded thereby
; FILE REFERENCE: 2750-1590P052
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ. ID NOS: 119966
; SEQ. ID NO 45993
; LENGTH: 668
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1) .. (668)
; OTHER INFORMATION: Ceres Seq. ID no. 12600202
; US-11-056-355B-45993

```

Query Match	3.9%	Score	108	DB	7	Length	668
Best Local	Similarity	18.6%	Pred	No.2.2			
Matches	97	Conservative	81	Mismatches	178	Indels	166
						Gaps	24

[illegible]

```

RESULT 12
US-11-056-355B-45992
; Sequence 45992, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 45992
; LENGTH: 676.
; TYPE: p1t
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(676)
; OTHER INFORMATION: Ceres Seq. ID no. 12600201
; US-11-056-355B-45992

```

Query Match	3.9%	Score 108;	DB 7;	Length 676;
Best Local Similarity	18.6%	Pred. No. 2.3;		
Matches 97;	Conservative 81;	Mismatches 178;	Indels 166;	Gaps 24;

```

QY 74 SVSSAASTBDSDDDEVPREKQQTNSNGSSNFCYKINIKOAEFORRELEIAOQMSALIS 133
Db 56 SSSSSASGSHLRLNHLICRRRTTNQNNNGVAQYFYKGGKKELANER---IKDEVLSSVNV 112
QY 134 RKRAQGEK-----PLAGAKIVGCTHTTAQTAIVLIER 164
Db 113 REHEKEHEDEVNVVSGLDORRCFEDLANMILHGGYPLSVSDVDGGRNFIQNLQPLFEL 172

```

QY 165 LC--ALGACRWSACNISTQ-NEVAAL-----AAGVAVFAMKGESEDDFMWCIDRCVN 217
 DB 173 VAEERVESDC-----MEIYAKEKHIFALDLPKGISISVDVWSSGSDSEFLCL----- 223
 QY 218 MDGQAMMILDDGDLTHWVYKKYPNFKIRGIVESVTGV-----HR 261
 DB 224 -----AAHYIDEGWEIK-----KRVLNFF-----MVDPSHSGEMLAEVIMTCLMEMWIDRK 269
 QY 262 LYOLSKAGKLCVP-----AMVNDVSTKOKFNDLYCCRESIIDGLKRTTDMFGKQOVV 316
 DB 270 LF--SWASSHAPPSSENVASKIRDRLSQNKF--LYC-----YQGLPDSV 309
 QY 317 CGYGEVG-----KCCCALAKAL-GAIYITEIDIPICALQACMDGFRVVKLNEVIRVD 368
 DB 310 CGVNVINEMVQDSLACCCTDITINIRRESIRYKSSSEI-----QDRF-----NOMIVETG 358
 QY 369 VV-----ITCTGNKVVTREHLDRMKSCICVCMNGHSTELIDVTSLRTP-E 413
 DB 359 AVSERNLICIDDPKRWSTCTMLENALRQKSAFSLMN-----EHPDPSVLCPSD 406
 QY 414 LTVERRVSOVDHVIWPDGKRVLLAEGRLNLSCSTVPFVLSTATTQALALIELYNAP 473
 DB 407 LEWERLGTIVEFL-----KVFEVINAFTKSSC--LPANMYPEVCDIHLRLIEMSKNP 458
 QY 474 EGRYKODVYLLPKKMEY-----VASLHLPSPDAHLTE 506
 DB 459 DDFISSLVNMRKKFDDFMDKNYLVLAITLDPREFRMKLV 500

RESULT 13
 US-11-056-355B-88620
 ; Sequence 88620, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander, Vyacheslav
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 88620
 ; LENGTH: 716
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(716)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12711171
 US-11-056-355B-88620

Query Match 3.9%; Score 108; DB 7; Length 716;
 Best Local Similarity 18.6%; Pred. No. 2.5;
 Matches 97; Conservative 81; Mismatches 178; Indels 166; Gaps 24;

QY 74 SYSSAASYDSSDEVSPPREKQOTNSKGSNFCVNKIKOAFGRREIEIAEQMSALISL 133
 DB 96 SGSSASGTSHLRNHLIRCRRTGNNGNVAQYFVKGGKKELANER---IKDEVLSTVNV 152
 QY 134 RKRAQGEK-----PLAGAKIVGCTHTTAOTAVLIET 164
 DB 153 RYHEKEHEHDVNVVSMGLDORCRFDLARMITLHGYPPLSMVEDVGRMFIGNLQPLFEL 212
 QY 165 LC--ALGACRWSACNISTQ-NEVAAL-----AAGVAVFAMKGESEDDFMWCIDRCVN 217
 DB 213 VAEERVESDC-----MEIYAKEKHIFALDLPKGISISVDVWSSGSDSEFLCL----- 263
 QY 218 MDGQAMMILDDGDLTHWVYKKYPNFKIRGIVESVTGV-----HR 261

DB 264 -----AAHYIDEGWEIK-----KRVLNFF-----MVDPSHSGEMLAEVIMTCLMEMWIDRK 309
 QY 262 LYOLSKAGKLCVP-----AMVNDVSTKOKFNDLYCCRESIIDGLKRTTDMFGKQOVV 316
 DB 310 LF--SWASSHAPPSSENVASKIRDRLSQNKF--LYC-----YQGLPDSV 349
 QY 317 CGYGEVG-----KCCCALAKAL-GAIYITEIDIPICALQACMDGFRVVKLNEVIRVD 368
 DB 350 CGVNVINEMVQDSLACCCTDITINIRRESIRYKSSSEI-----QDRF-----NOMIVETG 358
 QY 369 VV-----ITCTGNKVVTREHLDRMKSCICVCMNGHSTELIDVTSLRTP-E 413
 DB 399 AVSERNLICIDDPKRWSTCTMLENALRQKSAFSLMN-----EHPDPSVLCPSD 446
 QY 414 LTVERRVSOVDHVIWPDGKRVLLAEGRLNLSCSTVPFVLSTATTQALALIELYNAP 473
 DB 447 LEWERLGTIVEFL-----KVFEVINAFTKSSC--LPANMYPEVCDIHLRLIEMSKNP 498
 QY 474 EGRYKODVYLLPKKMEY-----VASLHLPSPDAHLTE 506
 DB 499 DDFISSLVNMRKKFDDFMDKNYLVLAITLDPREFRMKLV 540

RESULT 14
 US-11-056-355B-92376
 ; Sequence 92376, Application US/11056355B
 ; Publication No. US20060150283A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexander, Vyacheslav
 ; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
 ; FILE REFERENCE: 2750-1590PUS2
 ; CURRENT APPLICATION NUMBER: US/11/056,355B
 ; CURRENT FILING DATE: 2005-02-14
 ; PRIOR APPLICATION NUMBER: 60/544,190
 ; PRIOR FILING DATE: 2004-02-13
 ; NUMBER OF SEQ ID NOS: 119966
 ; SEQ ID NO 92376
 ; LENGTH: 716
 ; TYPE: prt
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: peptide
 ; LOCATION: (1)..(716)
 ; OTHER INFORMATION: Ceres Seq. ID no. 12711171
 US-11-056-355B-92376

Query Match 3.9%; Score 108; DB 7; Length 716;
 Best Local Similarity 18.6%; Pred. No. 2.5;
 Matches 97; Conservative 81; Mismatches 178; Indels 166; Gaps 24;

QY 74 SYSSAASYDSSDEVSPPREKQOTNSKGSNFCVNKIKOAFGRREIEIAEQMSALISL 133
 DB 96 SGSSASGTSHLRNHLIRCRRTGNNGNVAQYFVKGGKKELANER---IKDEVLSTVNV 152
 QY 134 RKRAQGEK-----PLAGAKIVGCTHTTAOTAVLIET 164
 DB 153 RYHEKEHEHDVNVVSMGLDORCRFDLARMITLHGYPPLSMVEDVGRMFIGNLQPLFEL 212
 QY 165 LC--ALGACRWSACNISTQ-NEVAAL-----AAGVAVFAMKGESEDDFMWCIDRCVN 217
 DB 213 VAEERVESDC-----MEIYAKEKHIFALDLPKGISISVDVWSSGSDSEFLCL----- 263
 QY 218 MDGQAMMILDDGDLTHWVYKKYPNFKIRGIVESVTGV-----HR 261
 DB 264 -----AAHYIDEGWEIK-----KRVLNFF-----MVDPSHSGEMLAEVIMTCLMEMWIDRK 309
 QY 262 LYOLSKAGKLCVP-----AMVNDVSTKOKFNDLYCCRESIIDGLKRTTDMFGKQOVV 316
 DB 310 LF--SWASSHAPPSSENVASKIRDRLSQNKF--LYC-----YQGLPDSV 349
 QY 317 CGYGEVG-----KCCCALAKAL-GAIYITEIDIPICALQACMDGFRVVKLNEVIRVD 368

```

Db      350 CGNNVNVENVQDLEACCDTINIRRESIRYKXSESI-----QDRF-----NQWIVETG 398
Qy      369 VV-----ITGTGNKNVVTREHLDRMKNSCIYCNNGHSNTIEDVTSLRT-P-E 413
Db      399 AVSERNLICIDDPMRWDSTCTMLENALEQKSAFSLMN-----EHDPPSVLCPSD 446
Qy      414 LTMERVSQVDHYIWDGKRVVLLAEGRLNLSCSTVPFVLSITATQALALIELYNAP 473
Db      447 LEMERLGTIVEFL-----KVFEVINAFTKSSC--LPANMYPEVCDIHLRLIEMSKNP 498
Qy      474 EGRYKQDVYLLPKKMDXY-----VASLHLPSPDAHYTE 506
Db      499 DDFISLVVNMKRTDPPFMDKNYLVLAIALIILDPREFRMKLVE 540

```

```

RESULT 15
US-11-056-355B-88619
; Sequence 88619, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 88619
; LENGTH: 720
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(720)
; OTHER INFORMATION: Ceres Seq. ID no. 12711170
US-11-056-355B-88619

```

Query Match Best Local Similarity 18.6%; Score 108; DB 7; Length 720; Matches 97; Conservative 81; Mismatches 178; Indels 166; Gaps 24;

```

Qy      74 SYSSAASYDSSDDEVSPREKQTSKSSNFCVKNIKQAEFRREIEIAEODMSALISL 133
Db      100 SSSASAGTSHLRNHLIRCRRTGNNGVAVQYFVGKKELANER--IKDEVLISVVNV 156
Qy      134 RRAQGEK-----PLAGAKIVGCTHTTAQTAVLIET 164
Db      157 RYEHKEHEHEDVNVVSMGLDQRRCPDLARMILHGYPLSMVEDVGFPMFIGNLOPLFEL 216
Qy      165 LC--ALGAQCRWSACNIYSTQ--NEVAAAL--AEAGVAVFAVKGESEDDFWMCIDRCVN 217
Db      217 VAFERYESDC---MEIYAKEKIKIFEALDKLPKGISISVDVWSSGSDSDEFCLT----- 267
Qy      218 MDGMOANMILDDGGDITHWVYKYPNVFKKIRGIVEESVTGV-----HR 261
Db      268 -----AAHYIDSGWELK---KVLNFF-----MVDPSHSGEMLAEVIMTCLMEWDIDRK 313
Qy      262 LYQLSAGKLCVP-----AMNVNDSTYKQKFDNLVCCRESILDGLKRTDVMFGKQVYV 316
Db      314 LF--SWASSHAPFSSENVASKIRDRLSQNF--LYC-----YGOLFVVS 353
Qy      317 CGYGEVG-----KGCALALKAL--GAIYVITEIDPICALQACMDGFRVVKLNEVIRQVD 368
Db      354 CGVNVVNEWQDSLEACCTINIRRESIRYKXSESI-----QDRF-----NQWIVETG 402
Qy      369 VV-----ITGTGNKNVVTREHLDRMKNSCIYCNNGHSNTIEDVTSLRT-P-E 413
Db      403 AVSERNLICIDDPMRWDSTCTMLENALEQKSAFSLMN-----EHDPPSVLCPSD 450

```

```

Qy      414 LTMERVSQVDHYIWDGKRVVLLAEGRLNLSCSTVPFVLSITATQALALIELYNAP 473
Db      451 LEMERLGTIVEFL-----KVFEVINAFTKSSC--LPANMYPEVCDIHLRLIEMSKNP 502
Qy      474 EGRYKQDVYLLPKKMDXY-----VASLHLPSPDAHYTE 506
Db      503 DDFISLVVNMKRTDPPFMDKNYLVLAIALIILDPREFRMKLVE 544

```

Search completed: September 6, 2006, 19:58:38
Job time : 32.5326 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:15:08 ; Search time 43.2826 Seconds
(without alignments)
1161.987 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_110
Perfect score: 555
Sequence: 1 MSMFDPMLPGVGBELKQAK.....PREKQNTSKSSNFCVKNIT 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000,

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- A_Geneseq_8:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1990s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2004s:*
 - 8: Geneseqp2005s:*
 - 9: Geneseqp2006s:*
 - 10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	100.0	239	3	AAB56801 Human pro
2	555	100.0	530	7	ADB68448 Human DCA
3	555	100.0	530	7	ADB68450 Murine DC
4	555	100.0	530	7	ADB68452 Murine DC
5	555	100.0	530	7	ADB68446 Human DCA
6	555	100.0	530	8	ADM94432 Mouse ino
7	555	100.0	530	8	ABM80118 Tumour-as
8	555	100.0	530	8	ADP23045 PRO polyp
9	555	100.0	614	2	AAW56097 Amino aci
10	401	72.3	500	2	AAW90061 Human SAH
11	356	64.1	597	8	ADO43989 Amino aci
12	329	59.3	611	8	ABM80935 Tumour-as
13	322.5	58.1	455	4	ABG12029 Novel hum
14	307	55.3	564	5	ABG32171 Novel hum
15	302	54.4	508	8	ADSI0638 Human enz
16	302	54.4	509	8	ADL90193 Human enz
17	157.5	28.4	521	4	ABBS8663 Drosophil
18	104	18.7	504	4	ABBT7110 Drosophil
19	87	15.7	2296	8	ADN60280 Human spl
20	86.5	15.6	414	2	AAW10529 Saccharom
21	86.5	15.6	414	4	AAAB30809 Amino aci
22	86.5	15.6	414	10	ABE28461 Yeast nuc
23	86.5	15.6	414	10	ABE72826 S. cerevi

24	86	15.5	419	8	ADR86387	Adt86387 Aspergill
25	86	15.5	446	8	ADR86528	Adt86528 Aspergill
26	86	15.5	584	8	ADR86515	Adt86515 Aspergill
27	85	15.3	1788	8	ADO17144	Novel exp
28	83.5	15.0	2058	8	ADM48570	Adm48570 Ankyrin r
29	83	15.0	628	8	ADS44146	AdS44146 Bacterial
30	82.5	14.9	333	4	ABBS8754	Abb68754 Drosophil
31	81.5	14.7	428	5	ABG93245	Abg93245 C. albica
32	81	14.6	1499	4	AAW42018	AAW42018 Human pol
33	80	14.4	240	9	AEA28149	Aea28149 Sericin p
34	80	14.4	640	9	ADK62830	Adk62830 Disease t
35	79.5	14.3	156	3	ABAB3709	AbA3709 Human can
36	79.5	14.3	176	4	ABBT71395	Abb71395 Drosophil
37	79.5	14.3	220	7	ADCC3148	AdC33148 Human nov
38	79.5	14.3	1791	6	ABO52986	ABO52986 Human put
39	79.5	14.3	2752	8	ADN60298	Adn60298 Human ser
40	79.5	14.3	2752	8	ADP24102	Adp24102 PRO polyp
41	79.5	14.3	2752	9	ADY91619	AdY91619 Human pro
42	79	14.2	948	7	ADE34334	AdS34334 Retinobla
43	79	14.2	948	8	ADK67723	Adk67723 Human mod
44	79	14.2	948	8	ADK60419	Adk60419 Angiogene
45	79	14.2	948	8	ADK60720	Adk60720 Angiogene

ALIGNMENTS

RESULT 1	ABBS6801	ABBS6801 standard; protein; 239 AA.
ID	ABBS6801	
XX	XX	
AC	ABBS6801	
XX	XX	
DT	13-MAR-2001	(first entry)
XX	XX	
DE	Human prostate cancer antigen protein sequence SEQ ID NO:1379.	
XX	XX	
KW	Human; prostate cancer; prostate cancer antigen; detection; diagnosis;	
KW	neuroprotective; cytoskeletal; cardioactive; immunomodulatory; muscular;	
KW	vulnary; gastrointestinal; nephrotoxic; antiinfective; gynaecological;	
KW	antibacterial; gene therapy; neural; immune; reproductive; renal;	
KW	gastrointestinal; pulmonary; cardiovascular; proliferative disorder;	
KW	wound; infectious disease.	
OS	Homo sapiens.	
XX	XX	
PN	MO200055174-A1.	
XX	XX	
PD	21-SEP-2000.	
XX	XX	
PF	08-MAR-2000; 2000MO-US005988.	
XX	XX	
PR	12-MAR-1999; 99US-0124270P.	
XX	XX	
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX	XX	
PA	(ROSE/) ROSEN C A.	
XX	XX	
PI	Rosen CA, Ruben SM;	
XX	XX	
DR	WPI: 2000-587513/55.	
XX	XX	
DR	N-PSDB: AAF16004.	
XX	XX	
PT	Prostate cancer associated gene sequences, referred to as prostate cancer	
XX	XX	
PT	antigens, useful for treatment, prevention, and diagnosis of disorders	
XX	XX	
XX	such as prostate cancer.	
PS	Claim 11; Page 1803-1804; 2338pp; English.	
XX	XX	
CC	AAFI5566 to AAF16505 encode the human prostate cancer associated	
CC	proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.	
CC	The prostate cancer antigens can have neuroprotective, cytoskeletal,	
CC	cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,	
CC	nephrotoxic, antiinfective, gynaecological and antibacterial activities,	

CC and can be used in gene therapy. The prostate cancer antigen
CC polynucleotides may be used for detection of prostate cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The prostate cancer antigens may be used to treat
CC disorders such as neural, immune, muscular, reproductive,
CC gastrotestinal, pulmonary, cardiovascular, renal, and proliferative
CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
CC AAB57303 represent sequences used in the exemplification of the present
CC invention

XX Sequence 239 AA;

Query Match 100.0%; Score 555; DB 3; Length 239;
Best Local Similarity 100.0%; Pred. No. 6e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDMPPLPGVGEELKQAKETEDAKYSFMATVTAKPKKQIQFADDMQEFPTKTKGR 60
DB 86 MSMPDMPPLPGVGEELKQAKETEDAKYSFMATVTAKPKKQIQFADDMQEFPTKTKGR 145

QY 61 RLSLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNI 110
DB 146 RLSLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNI 195

RESULT 2

ADB68448
ID ADB68448 standard; protein; 530 AA.

XX ADB68448;

DT 04-DEC-2003 (first entry)

DE Human DCAL protein - SEQ ID 4.

KW dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
KW DC; AHcy; DCAL; anti-allergic; immunosuppressive; allergy; asthma;
KW allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
KW rheumatoid arthritis; transplant rejection; vaccine; gene therapy; human.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Domain 1..106 /note = Hydrophilic domain

FT Domain 107..530 /note = adenosine-homocysteine hydrolase (AHcy)-like

FT Binding-site 318..323 domain
/note= "NAD+ binding motif (GXGXXG)"

WO2003055997-A1.

PD 10-JUL-2003.

PF 24-DEC-2002; 2002WO-AU001761.

PR 24-DEC-2001; 2001AU-00009741.

PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.

PI Kato M, Angel NZ, Cooper BJ, Hart DNJ;

DR N-PSDB; ADB68445, ADB68447.

WIPI: 2003-559275/52.

PT New dendritic cell expressed S-adenosyl homocysteine hydrolase-like
PT molecule (DCAL) gene, useful for preparing a composition for treating or
PT preventing a condition e.g., allergy, autoimmune disease or transplant
PT rejection.

PS Disclosure; Fig 1B; 189pp; English.

CC The invention relates to a novel isolated polynucleotide comprising a
CC dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHcy)-
CC like molecule (DCAL) gene. The polynucleotide of the invention
CC demonstrates anti-allergic and immunosuppressive activities and may be
CC useful for treating a condition including an allergy such as asthma,
CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
CC therapy procedures. The genetically modified animal or the identified
CC modulatory agent of the invention may be used in the study of immunity,
CC DC function, brain physiology or neuronal cell function. The current
CC sequence is that of the human DCAL protein (SEQ ID 4) of the invention
CC which is encoded by the human DCAL cDNA.

XX Sequence 530 AA;

Query Match 100.0%; Score 555; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDMPPLPGVGEELKQAKETEDAKYSFMATVTAKPKKQIQFADDMQEFPTKTKGR 60
DB 1 MSMPDMPPLPGVGEELKQAKETEDAKYSFMATVTAKPKKQIQFADDMQEFPTKTKGR 60

QY 61 RLSLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNI 110
DB 61 RLSLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNI 110

RESULT 3

ADB68450
ID ADB68450 standard; protein; 530 AA.

XX ADB68450;

DT 04-DEC-2003 (first entry)

DE Murine DCAL protein - SEQ ID 6.

KW dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
KW DC; AHcy; DCAL; anti-allergic; immunosuppressive; allergy; asthma;
KW allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
KW rheumatoid arthritis; transplant rejection; vaccine; gene therapy;
KW murine; mouse.

OS Mus sp.

FH Key Location/Qualifiers

FT Binding-site 318..323 domain
/note= "NAD+ binding motif (GXGXXG)"

WO2003055997-A1.

PD 10-JUL-2003.

PF 24-DEC-2002; 2002WO-AU001761.

PR 24-DEC-2001; 2001AU-00009741.

PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.

PI Kato M, Angel NZ, Cooper BJ, Hart DNJ;

DR N-PSDB; ADB68449.

WIPI: 2003-559275/52.

PT New dendritic cell expressed S-adenosyl homocysteine hydrolase-like
PT molecule (DCAL) gene, useful for preparing a composition for treating or
PT preventing a condition e.g., allergy, autoimmune disease or transplant
PT rejection.

PS Disclosure; Page 170-172; 189pp; English.

CC The invention relates to a novel isolated polynucleotide comprising a
CC dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-
CC like molecule (DCAL) gene. The polynucleotide of the invention
CC demonstrates antiallergic and immunosuppressive activities and may be
CC useful for treating a condition including an allergy such as asthma,
CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
CC therapy procedures. The genetically modified animal or the identified
CC modulatory agent of the invention may be used in the study of immunity,
CC DC function, brain physiology or neuronal cell function. The current
CC sequence is that of the murine DCAL protein (SEQ ID 6) of the invention
CC which is encoded by genomic DNA.
XX
SQ Sequence 530 AA;
Query Match 100.0%; Score 555; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
DB 1 MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
61 RLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNII 110
61 RLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNII 110
RESULT 4
ADB68452
ID ADB68452 standard; protein; 530 AA.
AC ADB68452;
XX 04-DEC-2003 (first entry)
XX
XX Murine DCAL protein - SEQ ID 8.
DE
XX dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
XX DC; AHCY; DCAL; antiallergic; immunosuppressive; allergy; asthma;
XX allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
XX rheumatoid arthritis; transplant rejection; vaccine; gene therapy;
XX murine; mouse.
XX Mus sp.
XX
XX Key Location/Qualifiers
XX Binding-site 318..323
XX /note= "NAD+ binding motif (GXGXXG)"
XX WO2003055997-A1.
XX 10-JUL-2003.
XX 24-DEC-2002; 2002WO-AU001761.
XX 24-DEC-2001; 2001AU-00009741.
XX (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX PA Kato M, Angel NZ, Cooper BJ, Hart DNU;
XX PI Kato M, Angel NZ, Cooper BJ, Hart DNU;
XX DR N-PSDB; ADB68451.
XX WPI; 2003-559275/52.
XX N-PSDB; ADB68451.
XX New dendritic cell expressed S-adenosyl homocysteine hydrolase-like
XX molecule (DCAL) gene, useful for preparing a composition for treating or
XX preventing a condition e.g., allergy, autoimmune disease or transplant
XX rejection.
XX Disclosure; Page 175-177; 189pp; English.

CC The invention relates to a novel isolated polynucleotide comprising a
CC dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-
CC like molecule (DCAL) gene. The polynucleotide of the invention
CC demonstrates antiallergic and immunosuppressive activities and may be
CC useful for treating a condition including an allergy such as asthma,
CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
CC therapy procedures. The genetically modified animal or the identified
CC modulatory agent of the invention may be used in the study of immunity,
CC DC function, brain physiology or neuronal cell function. The current
CC sequence is that of the murine DCAL protein (SEQ ID 8) of the invention
CC which is encoded by cDNA.
XX
SQ Sequence 530 AA;
Query Match 100.0%; Score 555; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
DB 1 MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
61 RLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNII 110
61 RLSRSISQSSSTDYSASAAYTDSDDDEVSPREKQOTNSKGSNFCVKNII 110
RESULT 5
ADB68446
ID ADB68446 standard; protein; 530 AA.
AC ADB68446;
XX 04-DEC-2003 (first entry)
XX
XX Human DCAL protein - SEQ ID 2.
DE
XX dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
XX DC; AHCY; DCAL; antiallergic; immunosuppressive; allergy; asthma;
XX allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
XX rheumatoid arthritis; transplant rejection; vaccine; gene therapy; human;
XX chromosome 1p21.1.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Binding-site 318..323
XX /note= "NAD+ binding motif (GXGXXG)"
XX WO2003055997-A1.
XX 10-JUL-2003.
XX 24-DEC-2002; 2002WO-AU001761.
XX 24-DEC-2001; 2001AU-00009741.
XX (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
XX PA Kato M, Angel NZ, Cooper BJ, Hart DNU;
XX PI Kato M, Angel NZ, Cooper BJ, Hart DNU;
XX DR N-PSDB; ADB68445; ADB68447.
XX WPI; 2003-559275/52.
XX N-PSDB; ADB68445; ADB68447.
XX New dendritic cell expressed S-adenosyl homocysteine hydrolase-like
XX molecule (DCAL) gene, useful for preparing a composition for treating or
XX preventing a condition e.g., allergy, autoimmune disease or transplant
XX rejection.

PT preventing a condition e.g., allergy, autoimmune disease or transplant
XX rejection.
PS Disclosure; Fig 1B; 189pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC dendritic cell (DC)-expressed 5'-adenosyl homocysteine hydrolase (AHCY)-
CC like molecule (DCLH) gene. The polynucleotide of the invention
CC demonstrates anti-allergic and immunosuppressive activities and may be
CC useful for treating a condition including an allergy such as asthma,
CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
CC therapy procedures. The genetically modified animal or the identified
CC modulatory agent of the invention may be used in the study of immunity,
CC DC function, brain physiology or neuronal cell function. The current
CC sequence is that of the human DCLH protein (SEQ ID 2) of the invention
CC which is encoded by DNA localised to chromosome 1p21.1.
XX
SQ Sequence 530 AA;
XX
Query Match 100.0%; Score 555; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MSMPDAMPVPGVGEELKQAKIEDEAKYSFMAVTYTKAPKKQIQFADDMQEFPTKTKGR 60
DB 1 MSMPDAMPVPGVGEELKQAKIEDEAKYSFMAVTYTKAPKKQIQFADDMQEFPTKTKGR 60
XX
OY 61 RLSRSISQSSSTDYSYSSAASYTSSDDEVSPREKQOTNSKSSNFCVXNI 110
DB 61 RLSRSISQSSSTDYSYSSAASYTSSDDEVSPREKQOTNSKSSNFCVXNI 110
XX
RESULT 6
ADM94432
ID ADM94432 standard; protein; 530 AA.
XX
AC ADM94432;
XX
DT 01-JUL-2004 (first entry)
XX
DE Mouse inositol 1,4,5-triphosphate receptor binding protein.
XX
KW inositol-triphosphate receptor-binding protein; IP3 receptor;
KW fluorescence resonance energy transfer; IP3 quantification;
KW IP3-induced Ca2+ releasing activity; PIP2 function.
XX
OS Mus musculus.
XX
PN EPI408049-A2.
XX
PD 14-APR-2004.
XX
PF 13-OCT-2003; 2003EP-00256457.
XX
PR 11-OCT-2002; 2002UP-00299429.
XX
PA (RIKE) RIKEN KK.
XX
PI Mikoshiba K, Ando H, Mizutani A, Matsu-Ura T;
XX
DR WPI; 2004-349314/33.
XX
DR N-PSDB; ADM94433.
XX
PT New inositol 1,4,5-triphosphate receptor-binding protein that binds to
PT inositol 1,4,5-triphosphate receptor; useful as inositol 1,4,5-
PT triphosphate indicator intracellularly and in cell-free system.
XX
PS Claim 1; SEQ ID NO 1; 61pp; English.
XX
CC The invention relates to a novel inositol 1,4,5-triphosphate (IP3)
CC receptor-binding protein (I) that binds to IP3 receptor. (I) is used as

CC an IP3 indicator in combination with a fluorescent molecule for detecting
CC IP3 by the fluorescence resonance energy transfer (FRET) method using a
CC combination of two fluorescent molecules applicable to the FRET method,
CC and a protein containing at least IP3-binding domain of IP3 receptor
CC labelled with the other fluorescent molecule. (I) is useful as IP3
CC indicator intracellularly and in cell-free system, for detecting and/or
CC quantifying IP3, as modulator of IP3-induced Ca2+ releasing activity,
CC modulator of PIP2 function and Na2+ and bicarbonate ions. This sequence
CC represents the IP3 receptor binding protein.
XX
SQ Sequence 530 AA;
XX
Query Match 100.0%; Score 555; DB 8; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 MSMPDAMPVPGVGEELKQAKIEDEAKYSFMAVTYTKAPKKQIQFADDMQEFPTKTKGR 60
DB 1 MSMPDAMPVPGVGEELKQAKIEDEAKYSFMAVTYTKAPKKQIQFADDMQEFPTKTKGR 60
XX
OY 61 RLSRSISQSSSTDYSYSSAASYTSSDDEVSPREKQOTNSKSSNFCVXNI 110
DB 61 RLSRSISQSSSTDYSYSSAASYTSSDDEVSPREKQOTNSKSSNFCVXNI 110
XX
RESULT 7
ABM80118
ID ABM80118 standard; protein; 530 AA.
XX
AC ABM80118;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO80619, SEQ.301.
XX
KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX
PA (GENTH) GENENTECH INC.
XX
PI Wu TD, Zhang Z, Zhou Y;
XX
DR WPI; 2004-347921/32.
XX
DR N-PSDB; ACN37426.
XX
PT New tumour-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
PS Claim 12; SEQ ID NO 301; 7273pp; English.
XX
CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and

CC polypeptides; expression vectors and host cells comprising a TAT nucleic acid; an antibody specific for a TAT polypeptide; a peptide or organic molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT polypeptide of the invention

CC SEQ Sequence 530 AA;

Query Match 100.0%; Score 555; DB 8; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 MSMPDAMPVGVGEELKQAKIEDEAKYSFMATVTKAPKKQIQFADDDQEFKPTKTCR 60
1 MSMPDAMPVGVGEELKQAKIEDEAKYSFMATVTKAPKKQIQFADDDQEFKPTKTCR 60

Db 61 RSLSRISISQSTDSYSSAASYTDSDDDEVSPREKQQTNSKSSNFCVKN 110
61 RSLSRISISQSTDSYSSAASYTDSDDDEVSPREKQQTNSKSSNFCVKN 110

ADP23045
ADP23045 standard; protein; 530 AA.

DT 18-NOV-2004 (first entry)

DE PRO polypeptide SEQ ID NO:139.

XX PRO; antiinflammatory; antirheumatic; antirheumatic; immunosuppressive;
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.

OS Unidentified.

PN WO2004041170-A2.

PD 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

DR N-PSDB; ADP23044.

XX WPI; 2004-419628/39.

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.

XX Claim 7; SEQ ID NO 139; 2940bp; English.

CC The invention relates to a novel isolated nucleic acid and the PRO
CC polypeptide encoded by it. A protein of the invention has
CC antiinflammatory, antirheumatic, antipneumatic, immunosuppressive,
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,

CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthritis, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
CC vasculitis, sarcoidosis, autoimmune haemolytic anemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantation associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.

CC SEQ Sequence 530 AA;

Query Match 100.0%; Score 555; DB 8; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 1 MSMPDAMPVGVGEELKQAKIEDEAKYSFMATVTKAPKKQIQFADDDQEFKPTKTCR 60
1 MSMPDAMPVGVGEELKQAKIEDEAKYSFMATVTKAPKKQIQFADDDQEFKPTKTCR 60

Db 61 RSLSRISISQSTDSYSSAASYTDSDDDEVSPREKQQTNSKSSNFCVKN 110
61 RSLSRISISQSTDSYSSAASYTDSDDDEVSPREKQQTNSKSSNFCVKN 110

AAW56097
AAW56097 standard; protein; 614 AA.

AC AAW56097;

DT 21-AUG-1998 (first entry)

DE Amino acid sequence of the ODD4b5.3 enzyme.

XX DD4b5.3 enzyme; S-adenosyl-L-homocysteine hydrolase-type activity;
KW AHCt-type activity; stimulation; inhibition; dendritic cell; cancer;
XX autoimmune disease; transplantation.

OS Homo sapiens.

XX WO9814562-A1.

XX 09-APR-1998.

XX 06-OCT-1997; 97WO-NZ000133.

XX 04-OCT-1996; 96NZ-00295507.

XX (HART/) HART D N J.

XX Hart DNU;

XX WPI; 1998-240074/21.

DR N-PSDB; AAW56097.

XX New isolated S-adenosyl-L-homocysteine hydrolase enzyme - is used to
PT develop products which can be used in the treatment of e.g. auto-immune
PT disease, transplantations or cancers.

XX PS Claim 3; Fig 1; 33pp; English.
XX CC This is the amino acid sequence of the DD4p9.3 enzyme which has S-
XX CC adenosyl-L-homocysteine hydrolase (AHCV)-type activity. Its products can
XX CC be used to identify substances which have a stimulatory or inhibitory
XX CC effect on the enzyme activity. Such substances can be used to modulate
XX CC dendritic cell (DC) function and for immunomodulation. They can be used
XX CC in the treatment of e.g. autoimmune diseases, transplantations or
XX CC cancers. The products can also be used for detection and diagnosis
XX SQ Sequence 614 AA;
XX
XX Query Match 100.0%; Score 555; DB 2; Length 614;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-54;
XX Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSMPDAMPLEGVGEELKQAEIEDEAKYSPATYTKAPKQIQADMOEFTKPTTGR 60
XX DB 85 MSMPDAMPLEGVGEELKQAEIEDEAKYSPATYTKAPKQIQADMOEFTKPTTGR 144
XX
XX QY 61 RSLSRISQSTSDSYSSAASYTDSDEVSPPREKQNTSKSSNFCVKNI 110
XX DB 145 RSLSRISQSTSDSYSSAASYTDSDEVSPPREKQNTSKSSNFCVKNI 194
XX
XX RESULT 10
XX ID AAW90061 standard; protein; 500 AA.
XX AC AAW90061;
XX DT 04-MAR-1999 (first entry)
XX DE Human SAHH protein.
XX DE
XX DE S-adenosyl-5-homocysteine hydrolase; SAHH; human; drug screening;
XX KW treatment; infection; cancer; autoimmune disease; detection; diagnosis;
XX KW gene mapping; antisense; therapy; antagonist; immunoassay.
XX OS Homo sapiens.
XX PN US854023-A.
XX PD 29-DEC-1998.
XX PF 17-JUL-1997; 97US-00896005.
XX PR 17-JUL-1997; 97US-00896005.
XX (INCY-) INCYTE PHARM INC.
XX PA Shah P, Lal P, Hillman JL, Corley NC;
XX PI WPI; 1999-094906/08.
XX DR N-PSDB; AAV73924.
XX
XX PT Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase - for
XX PT production of recombinant enzyme, useful for diagnosis, treatment and
XX PT prevention of cancers, infections and autoimmune diseases.
XX
XX PS Claim 1; Fig 1A-I; 40pp; English.
XX
XX CC This sequence represents a human S-adenosyl-5-homocysteine hydrolase
XX CC (SAHH). The SAHH protein can be used to generate specific antibodies and
XX CC in drug screening to identify specific binding agents. Antagonists of the
XX CC protein are used to treat or prevent a wide range of viral, bacterial,
XX CC fungal, parasitic, protozoal or helminthic infections, many cancers
XX CC (leukaemia, lymphoma or solid tumours), and many autoimmune diseases
XX CC (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes
XX CC mellitus, multiple sclerosis etc). All these conditions may be treated by
XX CC expressing antisense sequences, triplex-forming agents or ribozymes
XX CC directed against the nucleic acid. The nucleic acid and its fragments can

CC be used as probes or primers for detecting and quantifying gene
CC expression, for diagnosis or monitoring of disease, to identify genetic
CC variations, mutations or polymorphisms, in gene mapping and as antisense
CC therapeutics. Antibodies are used directly as antagonists, indirectly to
CC deliver active agents to SAHH-expressing cells, to diagnose and monitor
CC diseases in standard immunoassays, in competitive drug screens and to
XX CC isolate the protein from natural sources
XX SQ Sequence 500 AA;
XX
XX Query Match 72.3%; Score 401; DB 2; Length 500;
XX Best Local Similarity 100.0%; Pred. No. 7.7e-37;
XX Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 31 MATVTAPKKQIQFADMOEFTKPTTGRSRISQSTSDSYSSAASYTDSDEVS 90
XX DB 1 MATVTAPKKQIQFADMOEFTKPTTGRSRISQSTSDSYSSAASYTDSDEVS 60
XX
XX QY 91 PREKQNTSKSSNFCVKNI 110
XX DB 61 PREKQNTSKSSNFCVKNI 80
XX
XX RESULT 11
XX ID ADO43989 standard; protein; 597 AA.
XX AC ADO43989;
XX DT 15-JUL-2004 (first entry)
XX DE Amino acid sequence of human putative S-adenosylhomocysteinease.
XX DE
XX DE protein complex; neurological disease; stroke; neurodegeneration;
XX KW Wallerian degeneration; Alzheimer's disease; neurological disorder;
XX KW epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;
XX KW atherosclerosis; 1D-WYO-inositol triphosphate 3 kinase A; ASK1; ASK2;
XX KW ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha;
XX KW Cdc37; CHK2; CTCL tumour antigen SE20-4; Ef-1 alpha 1; EMAP;
XX KW Fbj14653 NT2RP2002252; Fbj30839 FEBRA2002429; HBRCC2;
XX KW inositol polyphosphate-5-phosphatase; inositol-1; 4;
XX KW 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;
XX KW Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;
XX KW Pushover; S-adenosylhomocysteinease;
XX KW secretory carrier-associated membrane protein 2; surfactant locus protein 2;
XX KW ubiquitin carboxyl terminal hydrolase 11;
XX KW upstream regulatory element binding protein 1; Vartul;
XX KW Werner's syndrome helicase interacting protein; WHIP;
XX KW X-ray repair cross complementing protein 4.
XX OS Homo sapiens.
XX PN WO2004031242-A2.
XX PD 15-APR-2004.
XX PF 11-SEP-2003; 2003WO-EP010110.
XX PR 12-SEP-2002; 2002EP-00020495.
XX PR 12-SEP-2002; 2002EP-00020496.
XX PR 12-SEP-2002; 2002EP-00020497.
XX (CELL-) CELLZONE AG.
XX PA Boumeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;
XX PI Kuester B, Hopf C;
XX DR WPI; 2004-316467/29.
XX
XX CC New complex comprising at least one first protein, and at least one
XX CC second protein, useful for treating stroke, Alzheimer's disease,
XX CC neurological disorders such as epilepsy, and inflammatory conditions such
XX CC as ulcerative colitis.
XX PT

XX PS Example; Page 191-193; 287pp; English.

XX CC The specification describes protein complexes involved in cellular

XX CC processes which have been shown to be critical for the development of

XX CC various forms of neurological diseases. Three protein complexes were

XX CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3

XX CC protein complex. The protein complex are useful for treating diseases and

XX CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,

XX CC Alzheimer's disease, neurological disorders such as epilepsy, and

XX CC inflammatory conditions such as ulcerative colitis, Crohn's disease or

XX CC atherosclerosis. Proteins identified as being part of the protein

XX CC complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,

XX CC ASK1, ASK2, ASK3, CAMKII beta, CAMKII delta, CAMKII gamma, casein kinase

XX CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, Ef-1 alpha 1, EMAP,

XX CC FLJ14653, NTR2002252, FLJ30839, FEBRA202429, HERC2, two hypothetical

XX CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,

XX CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441,

XX CC MSTP030, Nek9, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1

XX CC precursor, Pushover, a putative S-adenosylhomocysteine, secretory

XX CC carrier-associated membrane protein 2, surfactant protein 2, ubiquitin

XX CC carboxyl terminal hydrolase 11, upstream regulatory element binding

XX CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),

XX CC X-ray repair cross complementing protein 4 (isoform 1). The present

XX CC sequence represents putative S-adenosylhomocysteine.

XX SQ Sequence 597 AA;

Query Match 64.1%; Score 356; DB 8; Length 597;

Best Local Similarity 56.6%; Pred. No. 1.4e-31;

Matches 82; Conservative 8; Mismatches 19; Indels 36; Gaps 4;

OY 1 MSMPAMLP-----GVGE--ELKQAKIEDAKYSFMATVTKAPK----- 40

DB 34 ISQP-ALPLPOTQAPSGESENLRNLROGRASSQNLSTLRILVSAQNGRDMRWLMI 92

OY 41 -----QIQFADDMOEFPTKPTGRRSLRSISOSSTSYSSAASYDSS 85

DB 93 QLMPEIDSLSEISCFIQIQFADDMOEFPTKPTGRRSLRSISOSSTSYSSAASYDSS 152

OY 86 DDEVSPREKQOTNSKGSNFCVKNI 110

DB 153 DDEVSPREKQOTNSKGSNFCVKNI 177

RESULT 12

ABM80935

ID ABM80935 standard; protein; 611 AA.

XX AC ABM80935;

XX DT 18-NOV-2004 (first entry)

XX DE Tumour-associated antigenic target (TAT) polypeptide PRO81608, SEQ.2410.

XX KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;

XX KM tumour; diagnosis; cell proliferative disorder; breast cancer;

XX KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;

XX KM central nervous system cancer; bladder cancer; pancreatic cancer;

XX KM cervical cancer; melanoma; leukaemia; hybridisation probe;

XX KM chromosome identification; chromosome mapping; gene mapping;

XX KM gene therapy; cytostatic.

XX OS Homo sapiens.

XX PN WO2004030615-A2.

XX PD 15-APR-2004.

XX PF 29-SEP-2003; 2003WO-US028547.

XX PR 02-OCT-2002; 2002US-0414971P.

XX XX

PA (GETH) GENENTECH INC.

XX PI Wu TD, Zhang Z, Zhou Y;

XX DR WPI; 2004-347921/32.

XX DR N-PSDB; ACN38718.

XX PT New tumor-associated antigenic target polypeptides and nucleic acids,

XX PT useful in preparing a medicament for treating or detecting a

XX PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or

XX PT prostate cancer or tumor.

XX PS Claim 12; SEQ ID NO 2410; 7273pp; English.

XX CC The invention relates to human tumour-associated antigenic target (TAT)

XX CC polypeptides, and their related nucleic acids. The TAT polypeptides are

XX CC overexpressed in cancer tissues compared to normal tissues, and may thus

XX CC serve as effective targets for the diagnosis and treatment of cancer in

XX CC mammals. The invention also relates to nucleic acid and polypeptide

XX CC sequences at least 80% identical to the TAT nucleic acids and

XX CC polypeptides; expression vectors and host cells comprising a TAT nucleic

XX CC acid; an antibody specific for a TAT polypeptide; a peptide or organic

XX CC molecule which binds to a TAT polypeptide; fusion proteins comprising a

XX CC TAT polypeptide; and methods and compositions for the treatment or

XX CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,

XX CC antibodies, antagonists, binding molecules and compositions are useful

XX CC for diagnosing or treating a cell proliferative disorder associated with

XX CC increased TAT expression, particularly cancers such as breast cancer,

XX CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder

XX CC cancer, pancreatic cancer, cervical cancer, cancers of the central

XX CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be

XX CC used as hybridisation probes, in chromosome and gene mapping, in

XX CC chromosome identification and in gene therapy. The present sequence

XX CC represents a TAT polypeptide of the invention

XX SQ Sequence 611 AA;

Query Match 59.3%; Score 329; DB 8; Length 611;

Best Local Similarity 57.3%; Pred. No. 1.9e-28;

Matches 75; Conservative 11; Mismatches 17; Indels 28; Gaps 3;

OY 8 PLPGVGE-----ELKQAKIEDAKY-----SFMATVTKAP---K 39

DB 61 PVPGSGPAAALSPAAGKVFQASAMKRSDPHHQHRDGGELVSPDGTVTEAPRVK 120

OY 40 KQIQFADDMOEFPTKPTGRRSLRSISOSSTSYSSAASYDSSDEVSPREKQOTNS 99

DB 121 KQIQFADDMOEFPTKPTGRRSLRSISOSSTSYSSAASYDSSDEVSPREKQOTNS 180

OY 100 KGSSNFCVKNI 110

DB 181 KGSSNFCVKNI 191

RESULT 13

ABG12029

ID ABG12029 standard; protein; 455 AA.

XX AC ABG12029;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #12020.

XX KM Human; chromosome mapping; gene mapping; gene therapy; forensic;

XX KM food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX XX

PF 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR N-PSDB; AAS76216.
XX
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 42388; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AB000010-AB030377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 455 AA;
SQ
Query Match 58.1%; Score 322.5; DB 4; Length 455;
Best Local Similarity 56.2%; Pred. No. 7e-28;
Matches 73; Conservative 13; Mismatches 17; Indels 27; Gaps 3;
QY 8 PLRQVGE-----ELKQKKEIEDAEKY-----SFMATYTKAKR--K 40
DB 61 PVPGGPSGPAALSPAGKVPQASAMKRSPPHQHQRHRDGGALVSPDQTVTEARTVK 120
QY 41 QIQFADMOEFTKPKTKGRSLRSRISOSSTDSYSSAASYTDSDEVS PREKQOTNSK 100
DB 121 KIQFADMOEFTKPKTKGRSLRSRISOSSTDSYSSAASYTDSDEVS PREKQOTNSK 180
QY 101 GSSNFCVKNK 110
DB 181 GSSDFCVKNK 190
RESULT 14
ABG32371
ID ABG32371 standard; protein; 564 AA.
XX
XX AC ABG32371;
XX
XX DT 15-NOV-2002 (first entry)
XX
XX Novel human enzyme, NZMS-1, Incyte 7484737CD1.
XX
XX Human; NZMS-1; immune system disorder; AIDS; contact dermatitis;
XX acquired immune deficiency syndrome; Chediak-Higashi syndrome;
XX common variable immunodeficiency; developmental disorder; cataract;
KW

KW Cushing's syndrome; hypothyroidism; eye disorder; glaucoma; asthma;
KW metabolic disorder; cystic fibrosis; sickle-cell anaemia; epilepsy;
KW smooth muscle disorder; lactic acidosis; neurological disorder;
KW Parkinson's disease; cardiac disorder; congestive heart failure;
KW myocardial infarction; pulmonary disorder; emphysema; bronchitis;
KW parasitic infection; amoebiasis; filariasis; cancer; leukaemia;
KW cell proliferative disorder; Incyte 7484737CD1; enzyme.
XX
XX Homo sapiens.
OS
PN MO200264795-A2.
XX
XX 22-AUG-2002.
PD
XX
XX 08-FEB-2002; 2002WO-US003814.
PF
XX
XX 09-FEB-2001; 2001US-0268113P.
PR 15-FEB-2001; 2001US-0268215P.
PR 27-FEB-2001; 2001US-0272271P.
PR 07-MAR-2001; 2001US-0274091P.
PR 09-MAR-2001; 2001US-0274423P.
PR 23-MAR-2001; 2001US-0278479P.
PR 23-MAR-2001; 2001US-0278480P.
XX
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Sanjanwala MM, Lu Y, Lee EA, Hafalia AJA, Warren BA, Baughn MR;
PI Tang TY, Yue H, Yao MG, Lee S, Thornton M, Wallia NK, Xu Y;
PI Tran UK, Lal PG, Lu DM, Swannaker A, Jones KA, Ring HZ;
XX
XX WPI; 2002-643486/69.
DR N-PSDB; ABR91312.
XX
XX
XX New isolated human enzymes (NZMS), useful for diagnosing, treating and
PT preventing immune system, developmental, eye, metabolic, smooth muscle,
PT neurological, pulmonary and cardiac disorders, cancer, or parasitic
PT infections.
XX
XX Claim 1; Page 147-149; 170pp; English.
XX
XX The invention relates to a new isolated human enzyme (NZMS) (I) and the
CC encoding nucleic acid (II). The polypeptides and polynucleotides are
CC useful in assessing the effects of exogenous compounds on the expression
CC of nucleic acid and amino acid sequences of NZMS. The NZMS or its
CC fragments are useful in screening compounds for effectiveness as agonist
CC or antagonist of the polypeptides, or in altering the expression of the
CC target polynucleotide and compounds that specifically bind to or modulate
CC the activity of the polypeptide. The antibody is useful in diagnosing a
CC condition or disease associated with the decreased expression or
CC overexpression of NZMS and in detecting (I). (I) is useful in the
CC production of antibodies. The microarray is useful in monitoring or
CC measuring gene expression profiles. The polypeptides and polynucleotides
CC are useful in diagnosing, treating and preventing diseases or conditions
CC associated with the decreased expression or overexpression of NZMS, such
CC as immune system disorders (e.g. acquired immune deficiency syndrome
CC (AIDS), contact dermatitis), immune deficiencies (e.g. common variable
CC immunodeficiency, Chediak-Higashi syndrome), developmental disorders
CC (e.g. Cushing's syndrome, hypothyroidism), eye disorders (e.g. glaucoma,
CC cataract), metabolic disorders (e.g. cystic fibrosis, sickle-cell
CC anaemia), smooth muscle disorders (e.g. asthma, lactic acidosis),
CC neurological disorders (e.g. Parkinson's disease, epilepsy), cardiac
CC disorders (e.g. congestive heart failure, myocardial infarction),
CC pulmonary disorders (emphysema, bronchitis), parasitic infections
CC (amoebiasis, filariasis), and cell proliferative disorders (e.g. cancer,
CC leukaemia). The microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions, and gene expression
CC profiles. The present sequence represents the amino acid sequence of one
CC of 11 novel human enzymes (NZMS1-11) of the invention
XX
XX Sequence 564 AA;
SQ
Query Match 55.3%; Score 307; DB 5; Length 564;
Best Local Similarity 75.0%; Pred. No. 5.6e-26;
KW

Matches 63; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Search completed: September 6, 2006, 19:21:45
Job time : 46.2826 secs

OY 27 KXSPATYTKAKKQIQFADDMQEFKPTKGRSLSSISQSSSTDSYSSAAYTDS 86
Db 61 KKKYIVNGNSGIRKQIQFADQKQEFKRPKTKIGRSLSSISQSSSTDSYSSAAYTDS 120
OY 87 DEVSPREKQOTNSKGSNFCVKN 110
Db 121 DETSPRDKQKNSKGSSDFCVKN 144

RESULT 15

ADSI0638
ID ADSI0638 standard; protein; 508 AA.

AC ADSI0638;

DT 16-DEC-2004 (first entry)

DE Human therapeutic protein - SEQ ID 875.

KW antiinflammatory; neuroprotective; antihaemic; cytostatic; vulnery;
inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
aplastic anaemia; cancer; wound healing; gene therapy.

OS Homo sapiens.

PN MO2004080148-A2.

PD 23-SEP-2004.

PF 30-SEP-2003; 2003WO-US030720.

PR 02-OCT-2002; 2002US-0416186P.

PA (NUVE-) NUVELO INC.

PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;

DR WPI; 2004-668857/65.

N-PSDB; ADS09954.

PT New polynucleotide, useful in preparing a composition for diagnosing or
treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
aplastic anemia or cancer for promoting wound healing.

PS Claim 20; SEQ ID NO 875; 718bp; English.

CC The invention relates to a novel isolated polynucleotide and the encoded
polypeptide. The molecules of the invention demonstrate antiinflammatory,
neuroprotective, antihaemic, cytostatic and vulnerary activities and may
be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
disorders, such as aplastic anaemia or cancer, as well as for promoting
wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
of the invention. The current sequence is not shown explicitly within the
specification but can be accessed from the WIPO web-site.

Sequence 508 AA;

Query Match 54.4%; Score 302; DB 8; Length 508;

Best Local Similarity 83.6%; Pred. No. 1.8e-25;

Matches 61; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

OY 38 PKKQIQFADDMQEFKPTKGRSLSSISQSSSTDSYSSAAYTDSDEVSPREKQOT 97
Db 16 PEMMIQFADQKQEFKRPKTKIGRSLSSISQSSSTDSYSSAAYTDSDEVSPRDKQOK 75

OY 98 NSKGSNFCVKN 110

Db 76 NSKGSDFCVKN 88

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:22:08 ; Search time 7.29348 Seconds
(without alignments)
1451.138 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_110

Perfect score: 555

Sequence: 1 MSMPPAMPPLPGVGEELKQAK.....PREKQOTNSKSSNFCVKNI 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	64.1	597	2	T08681 adenosylhomocysteine
2	104	18.7	527	1	S01302 adenosylhomocysteine
3	87	15.7	971	2	T19431 hypothetical prote
4	86.5	15.6	414	2	A39205 nuclear localizati
5	85.5	15.4	2717	2	A34203 DNA-binding protei
6	85	15.3	1788	2	T31095 vitellinogen precu
7	83.5	15.0	2038	2	A43742 female sterile hom
8	83	15.0	628	2	T39494 kinesin-like prote
9	82	14.8	542	2	F70220 conserved hypothet
10	81.5	14.7	788	2	T29768 probable membra
11	81.5	14.7	915	2	T16623 hypothetical prote
12	81.5	14.7	915	2	T16623 hypothetical prote
13	81	14.6	368	2	G88636 protein W09G12.7 (
14	81	14.6	1224	2	F96795 hypothetical prote
15	80	14.4	640	2	S48423 hypothetical prote
16	80	14.4	697	2	T16908 hypothetical prote
17	79.5	14.3	1791	2	T02345 hypothetical prote
18	79	14.2	271	2	A64923 hypothetical prote
19	79	14.2	948	2	A57440 retinolactoma bin
20	78.5	14.1	471	2	T33997 hypothetical prote
21	78	14.1	416	2	G81656 hypothetical prote
22	78	14.1	1067	2	T06312 hypothetical prote
23	77.5	14.0	651	2	T46050 hypothetical prote
24	77.5	14.0	898	2	T26577 hypothetical prote
25	77	13.9	406	2	S38170 SRP40 protein - ye
26	77	13.9	557	2	A96527 probable num1 prot
27	76.5	13.8	577	2	S30237 transactin init
28	76	13.7	233	2	T00966 hypothetical prote
29	76	13.7	271	2	D90924 probable lipoprote

30	76	13.7	271	2	H85772 probable lipoprote
31	76	13.7	734	2	G86171 hypothetical prote
32	76	13.7	754	1	UC5314 CDC28/cdc2-like K1
33	75.5	13.6	635	2	T09648 nucleolin homolog
34	75.5	13.6	860	2	UC4566 chitinase (EC 3.2.
35	75.5	13.6	918	2	T38786 transactin initiat
36	75.5	13.6	1359	2	T34036 hypothetical prote
37	75.5	13.6	1500	2	T03824 probable immediate
38	75.5	13.6	1507	2	B47328 natural killer cel
39	75	13.5	354	2	T06033 nucleocapsid prote
40	75	13.5	389	2	S08031 nucleolar protein
41	75	13.5	500	2	S55785 nucleolar phosphop
42	75	13.5	900	2	I51618 nucleolar phosphop
43	74.5	13.4	200	2	T25406 hypothetical prote
44	74.5	13.4	772	2	T06154 hypothetical prote
45	74.5	13.4	2688	2	I49477 alpha-A-crystallin

ALIGNMENTS

RESULT 1
T08681
adenosylhomocysteinease (EC 3.3.1.1) DKFZP564A1523 - human (fragment)
N/Alternate names: protein DKFZP564A1523.1
C/Species: Homo sapiens (man)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C/Accession: T08681
R/Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A/Reference number: Z16469
A/Accession: T08681
A/Molecule type: mRNA
A/Residues: 1-597 <MAN>
A/Cross-references: UNIPROT:O9UG84; UNIPARC:UPI000006FAA4; EMBL:AL049554
A/Experimental source: fetal brain; clone DKFZP564A1523
C/Genetics:
A/Note: DKFZP564A1523.1
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
C/Keywords: NAD; thioether hydrolase
F/379-408/Region: beta-alpha-beta NAD nucleotide-binding fold
F/244,278/Active site: Cys #status predicted

Query Match
Best Local Similarity 56.6%; Pred. No. 6.8e-25;
Matches 82; Conservative 8; Mismatches 19; Indels 36; Gaps 4;
QY 1 MSMPPAMPPLP-----GVGE---ELKQAKETEDAKESFMATVTKAPKK----- 40
34 ISQP-ALPLPQETQAPSGESENLRNLRQGRAESSQNLISRLVYSAONGRSDRWLMT 92
41 -----QIQFADDMQEFKPTKTRGRSLRSRISQGSTDSYSSAASYDSS 85
QY 93 QLMPEIDSLSEICFLQIQFADDMQEFKPTKTRGRSLRSRISQGSTDSYSSAASYDSS 152
Db 86 DDEVSPPREKQOTNSKSSNFCVKNI 110
153 DDEVSPPREKQOTNSKSSNFCVKNI 177

RESULT 2
S01302
adenosylhomocysteinease (EC 3.3.1.1) - fruit fly (Drosophila melanogaster)
C/Species: Drosophila melanogaster
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S01302
R/DeJorenzi, M.; Ali, N.; Saarl, G.; Henry, C.; Wilcox, M.; Blenz, M.
EMBO J. 7, 3222-3231, 1988
A/Title: Evidence that the Abdominal-B r element function is conferred by a trans-regulat
A/Reference number: S01302; MUID:89030618; PMID:2903049
A/Accession: S01302
A/Molecule type: DNA
A/Residues: 1-527 <DEL>

```

A:Cross-references: UNIPROT:P50245; UNIPARC:UPI000016B80E; EMBL:X13168; NID:g7675; PIDD:
C:Genetics:
A:Gene: FlyBase:Abd-B
A:Cross-references: FlyBase:FBgn0000015
A:Introns: 17/3; 4/1; 263/2; 369/3; 451/1
C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type
C:Keywords: NAD; thioether hydrolyase
P:275-304/Region: beta-alpha-beta NAD nucleotide-binding fold
P:140,174/Active site: Cys #status predicted

Query Match      18.7%   Score 104; DB 1; Length 527;
Best Local Similarity 50.0%; Pred. No. 0.069;
Matches 24; Conservative 9; Mismatches 13; Indels 2; Gaps 2;

OY 64 SRSTQSSTDYSSSAASTYDSDDE-VSPREKQNTNSKGSGSNFCVKN 110
    :|::||::||::||::||::||::||::||::||::||::||::||:
DB 27 ARRFDSVTGCSFSSYC-FTGSDEEDVAPKDHORNSAGGTDFCVKS 73

RESULT 3
T19431
hypothetical protein C25A1.10 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19431
R:Mortimore, B.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19124
A:Accession: T19431
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-971 <M1>
A:Cross-references: UNIPROT:O9XIS4; UNIPARC:UPI000007COA0; EMBL:Z81038; PIDD:CAB02755.1;
C:Genetics:
A:Experimental source: clone C25A1
C:Genetics:
A:Gene: CESP:C25A1.10
A:Map position: 1
A:Introns: 38/3; 92/3; 201/3; 919/3
C:Superfamily: nucleolin-cytoplasm shuttle phosphoprotein

Query Match      15.7%   Score 87; DB 2; Length 971;
Best Local Similarity 27.4%; Pred. No. 5;
Matches 37; Conservative 17; Mismatches 43; Indels 38; Gaps 6;

OY 4 PDAMPPLPG-----VGELKQAKETIEDAEK-----VSFMATVTKAPEK--QIQPADDM 48
DB 506 PAKPPTPANATPKPVAKKAESSSDSDDDEKKVPAKPTSATKATPPAKKADLSDFSDE 565
OY 49 QEFTEFPFKTGRRSLRSRISOSGSDTS-----YSSAASYTDSSD 87
DB 566 APAKTPKAAAPKPSK-K-AESSSDSDDDEKPAKSTPAKTTPKPYAKKAASSSDSSDD 624
OY 88 EVSPREKOOTNSKGS 102
    |::||::||::||::||::||::||::||::||::||::||::||:
DB 625 EKRPVAK-PTSAKAT 638

RESULT 4
nuclear localization sequence-binding protein NSRL - yeast (Saccharomyces cerevisiae)
A:Accession: A39205
N:Alternate names: nucleolar protein NSRL; p67 protein; protein G7001; protein YGR159c;
C:Species: Saccharomyces cerevisiae
C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 31-Dec-2004
C:Accession: A39205; PC2395; S60450; S64468; S64470
R:Lee, W.C.; Xue, Z.; Melese, T.
J Cell Biol. 113, 1-12, 1991
A>Title: The NSRL gene encodes a protein that specifically binds nuclear localization se
A:Reference number: A39205; MUID:51177946; PMID:1706724
A:Molecule type: DNA
A:Residues: 1-414 <LEE>
A:Cross-references: UNIPROT:P27476; UNIPARC:UPI0000035CF2; GB:X57185; NID:g4057; PIDD:CRK
R:Gamberi, C.; Contreas, G.; Romanelli, M.G.; Morandi, C.
```

Gene 148; 59-66; 1994
A>Title: Analysis of the Yeast NsrI gene and protein domain comparison between NsrI and I
A.Reference number: PC2395; MUID:95011659; PMID:7926838
A.Molecule type: mRNA
A.Accession: FC2395
A.Residues: 155-414 <GAM>
A.Cross-references: UNIPARC:UPI000017A377; EMBL:X57165
A>Note: The authors translated the codon TTC for residue 188 as Arg, GGT for residue 254
R.Skala, J.; Nawrocki, A.; Coffeau, A.
Yeast 11, 1421-1427, 1995
A>Title: The sequence of a 27 kb segment on the right arm of chromosome VII from Saccharr

A.Reference number: S60435; MUID:96158062; PMID:8585325
A.Accession: S60450
A>Status: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-114 <SKX>
A.Cross-references: UNIPARC:UPI0000035CF2; EMBL:X85807; NID:g1045249; PIDN:CAA5917.1; PJ
A.Note: The nucleotide sequence was submitted to the EMBL Data Library, March 1995
R.Van Dyck, L.; Skala, J.; de Wergilosse, P.; Purelle, B.; Talia, E.; Nawrocki, A.; Del
submitted to the Protein Sequence Database, May 1996
A.Reference number: S64428
A.Accession: S64468
A.Molecule type: DNA
A.Residues: 1-414 <VAN>
A.Cross-references: UNIPARC:UPI0000035CF2; EMBL:Z72944; NID:g1333270; PIDN:CAA97173.1; PI
A.Experimental source: strain 528BC
F.Rieger, M.; Mueller-Auer, S.; Bruechner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996
A.Reference number: S64071
A.Accession: S64470
A.Molecule type: DNA
A.Residues: 1-188 <RIE>
A.Cross-references: UNIPARC:UPI0000168F38; EMBL:Z72944; MIPS:YGR159C
A.Experimental source: strain 528BC
C.Genetics:
A.Gene: SGD:NSRI
A.Cross-references: SGD:S0003391; MIPS:YGR159C
A.Map position: 7R
C.Keywords: DNA binding; nucleus; RNA binding
F.165-236/Domains: ribonucleoprotein repeat homology <RRM1>
P.268-336/Domains: ribonucleoprotein repeat homology <RRM2>

Query Match

	Best local similarity	Score	% identity	Pred. No.	Mismatches	Gaps
Db	Matched	Conservative	Indels			
Oy	17 KOAKEIEAEKYSFMATVTKAPKKOIQPADMQEFPTKTGRSLRSISQSTDSYS	76	15.6%	DB 2	Length 414	
Db	18 KOKKE-EAKKAVSSSSSSSSSSSESESSESSESSESSESSEDSDSSES	76	31.4%	Pred. No. 2.1	39	Indices 15
Oy	77 -----SAASYTDDSDDEVSPREKOQT--NSKSASN 104	104	16	Mismatches 39	Indices 15	Gaps 3
Db	77 EAETKESKDSSSSDPSDEEEEEKETFKESKESISS 118	118				

RESULT 5

AJ3203
DNA-binding protein PRDI-BFI^{-/-}, human
A.Alternate names: major histocompatibility complex enhancer-binding protein 1
C.Species: Homo sapiens (man)
C.Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C.Accession: AJ3203; AJ4779
R.Fan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
A.Title: A DNA-binding protein containing two widely separated zinc finger motifs that re
A.Reference number: AJ3203; MUID:90169514; PMID:2106471
A.Accession: AJ3203
A.Status: Preliminary
A.Molecule type: mRNA
A.Residues: 1-2717 <NFAN>
A.Cross-references: UNIPROT:P15822; UNIPARC:UPI000013CA1; EMBL:X51435; NID:g38017; PIDN:

R.Baldwin Jr., A.S.; Leclaire, K.P.; Singh, H.; Sharp, P.A.

[illegible]

A:Gene: fish
A:Cross-references: FlyBase:FBgn0004656
C:Keywords: alternative splicing; transmembrane protein
F:1-2038/Product: female sterile homeotic protein, 205k #status predicted <MA2>
F:1-1106/Product: female sterile homeotic protein, 110k #status predicted <MA1>
F:59-116/Domain: bromodomain homology <BRO1>
F:503-560/Domain: bromodomain homology <BRO2>

Query Match 15.0%; Score 83.5; DB 2; Length 2038;
Best Local Similarity 28.1%; Pred. No. 25;
Matches 39; Conservative 16; Mismatches 45; Indels 39; Gaps 6;

OY 2 SMPDMPFPGVEBELKOA--KEIEDAEKYSFMATVTKAE---KKQIQADDMQEFTEK-FP 55
DB 989 SNPDIEID--FETLKPSTRLRLBSYVASCCLKAKTKHKKSGSKSDQMMEKQELEKRLQ 1046
OY 56 TKTGRRSLSR-----SIQGSSTDSYSSAASYTDS----- 86
DB 1047 DVTGGLGASKTKTAKKDESSAKVEAVQPANPVSSSSSSSSSSSSSSSSSSSSSSDSEAG 1106
OY 87 --DEVSPREKQOOTSNGSS 103
DB 1107 DGERPPRKKKSRDSNGSN 1125

RESULT 8
T39494
kinesin-like protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #ext_change 09-Jul-2004
C:Accession: T39494
R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, December 1998
A:Reference number: 221859
A:Accession: T39494
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-628 <BBC>
A:Cross-references: UNIPROT:O94732; UNIPARC:UPI000006C858; EMBL:AL034433; PIDN:CAA22353.1
C:Genetics:
A:Experimental source: strain 972h-, cosmid c1604
A:Gene: SPDB:SPBC1604.20C
A:Map position: 1

Query Match 15.0%; Score 83; DB 2; Length 628;
Best Local Similarity 28.6%; Pred. No. 7;
Matches 24; Conservative 21; Mismatches 23; Indels 16; Gaps 3;

OY 14 EELKAKIEDAEKYSFMATVTKAKKQIQPDDMQEFTKFPKTKRRSLRSISQSTP 73
DB 548 DELDPKEQIIYALRYA-----QKORDIADFNQSLAKFPKLIKKNVTRG-SRSSSD 597
OY 74 SYSASAYTDSDDDEVPREKQOT 97
DB 598 QFS-----NETKTEILPDDQOQS 615

RESULT 9
F70220
conserved hypothetical protein BBC05 - Lyme disease spirochete plasmid C/cp9
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #ext_change 09-Jul-2004
C:Accession: F70220
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Iathigra, R.; White, son, D.; Peterson, J.; Kurlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: F70220
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA

A:Residues: 1-302 <KLE>
A:Cross-references: UNIPROT:O50970; UNIPARC:UPI000005694A; GB:AE000791; NID:93253099; PI
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match 14.8%; Score 82; DB 2; Length 302;
Best Local Similarity 28.0%; Pred. No. 3.7;
Matches 28; Conservative 13; Mismatches 49; Indels 10; Gaps 3;

QY 7 MPELPGVEELKQAKEIEDAEKYSFMATVTKAPKQIQFADDMQEFKPTK--GRRSL 64
DB 28 MVLPGIDKMLKGV-----GVKGNFMEIAREIKKVIDKNLCLDFQFPFTIVGQV 82

QY 65 RSISQSTDSYSSAASYTDSDEVS PREKQOTNSGSSN 104
DB 83 HVV---RTTFYSTNTGYKDSFDPILTEMLKMNENSGKN 119

RESULT 10
S64030
probable membrane protein YGL028c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G3661
C:Species: Saccharomyces cerevisiae
C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 09-Jul-2004
C:Accession: S64030
R:Hebling, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64003
A:Accession: S64030
A:Molecule type: DNA
A:Residues: 1-542 <HEB>
A:Cross-references: UNIPROT:P53189; UNIPARC:UPI00001356BA; EMBL:Z72550; NID:91322499; PI
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:SCW11; MIPS:YGL028c
A:Cross-references: SGD:S0002996
A:Map position: 7L
C:Keywords: transmembrane protein
F:8-24/Domain: transmembrane #status predicted <TMM>

Query Match 14.7%; Score 81.5; DB 2; Length 542;
Best Local Similarity 26.7%; Pred. No. 8.1;
Matches 27; Conservative 20; Mismatches 45; Indels 9; Gaps 2;

QY 11 GVGEELKQAKEIEDAEKYSFMATVTKAPKQIQFADDMQEFK-----PFTKGRSL 63
DB 174 GVGEANVEGN--TQSGHMYQAATSTLMOQTSTIASQESTSTPTPTSSSTSS 231

QY 64 SRSISQSTDSYSSAASYTDSDEVS PREKQOTNSGSSN 104
DB 232 TSSSTSSSTSSSTSSSTSSSTSSSTSTSTSTSTSTSTSTSTSTSTSTSTSTSS 272

RESULT 11
T29768
hypothetical protein ZC581.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Dec-2004
C:Accession: T29768
R:Waterston, B.; Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid ZC581.
A:Reference number: Z20682
A:Accession: T29768
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-788 <WAT>
A:Cross-references: UNIPROT:O01772; UNIPARC:UPI0000179454; EMBL:AF003134; PTDN:AA854141.
A:Experimental source: strain Bristol N2; clone ZC581
C:Genetics:
A:Gene: CESP:ZC581.3
A:Map position: 1

A:Introns: 29/3; 66/3; 90/2; 109/2; 144/1; 223/2; 282/3; 351/3; 426/1; 590/3; 699/1

Query Match 14.7%; Score 81.5; DB 2; Length 788;
Best Local Similarity 25.7%; Pred. No. 13;
Matches 28; Conservative 19; Mismatches 39; Indels 23; Gaps 4;

QY 14 EELKQAKE-----IEAEKYSFMATVTKAPKQIQFADDMQEFK--PFTKGRSL 63
DB 263 EERKKEEERRRRIIDDEDEYSLRLKQVEETTVNVDDEDSYTKSTWTFEETNSL 322

QY 64 SRSISQSTDSYSSAAS-----YDSSDDEVSPREKQOTNS 99
DB 323 ESTSSSEFTASTSSISIPILGLTESIKQEDFTTLTDLTSAERPTER 371

RESULT 12
T16623
hypothetical protein M02D8.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16623
R:Miller, N.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid M02D8.
A:Reference number: Z18549
A:Accession: T16623
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-915 <ML>
A:Cross-references: UNIPROT:Q21461; UNIPARC:UPI0000081E0A; EMBL:U41034; NID:91086742; PI
A:Gene: CESP:M02D8.3
A:Introns: 29/2; 85/2; 102/2; 142/2; 189/2; 214/2; 230/2; 243/2; 286/2; 356/2; 610/1; 686

Query Match 14.7%; Score 81.5; DB 2; Length 915;
Best Local Similarity 24.6%; Pred. No. 15;
Matches 28; Conservative 15; Mismatches 50; Indels 21; Gaps 4;

QY 3 MPDMPLEGVGEELKQAKEIEDAEKYSFMATVTKAPKQ-----IQFADDMQEFKPT 56
DB 298 MPSPALPVP--TQSSSKSPRESSKEPKSLCPALNRSDDLPTQLAKYDENTDNSSSDLPR 356

QY 57 KTGRRSLRSISQSTDSYSSAASYTDSDEVS-----PREKQOTNSGSSN 104
DB 357 KTPRRSCVRGYKDLVDS-----DGEDEKKTAKMEKEXKTKKKEENN 402

RESULT 13
G88636
protein W09G12.7 (imported) - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88636
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: AT5000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A:Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88636
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <STO>
A:Cross-references: UNIPROT:O45198; UNIPARC:UPI000008159B; GB:chr_IV; PIDN:AA04447.1; P
C:Genetics:
A:Gene: W09G12.7
A:Map position: 4

Query Match 14.6%; Score 81; DB 2; Length 368;
Best Local Similarity 24.1%; Pred. No. 5.8;
Matches 21; Conservative 17; Mismatches 31; Indels 18; Gaps 1;

QY 36 KAPKQIQFADDMQEFKPT-----KTGRRLSRISQSTDSYSS 77

Db 25 KDKKTFEEEDVENVKRPFAESSDDEVVVVKKDQKRGKKKKPKKKQESSDDSSD 84
 Oy 78 AASYTSSDDEVSPREKQOTNSKSSN 104
 Db 85 NSDSSESSDDDKSKKKKKKKKKSSD 111

RESULT 14

F96795
 hypothetical protein F28016.9 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C:Accession: F96795
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Hultzer, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A66141; MUID:21016719; PMID:11130712
 A:Accession: F96795
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-1224 <STO>
 A:Cross-references: UNIPROT:Q9SRE1; UNIPARC:UPI00000A81ED; GB:AE005173; NID:g6143889; PI
 C:Genetics:
 A:Gene: F28016.9
 A:Map position: 1

Query Match 14.6%; Score 81; DB 2; Length 1224;
 Best Local Similarity 27.2%; Pred. No. 23;
 Matches 34; Conservative 23; Mismatches 46; Indels 22; Gaps 7;

Oy 4 PDAMPPLPGVGEELKQAKEIEDAEKYSF-----MATVT--KAPKKQIQPADDMQEFTEKP 55
 Db 28 PAASLAVG-ASCKKAVQSDDEEDKYSINTEBEKVITGKKKSNKKVYQKHDDDDDFTEAV 86
 Oy 56 TK--TGRRSLRSISQSTDSYS--SAASYTSS-----DDE--VSPREKQOTNSKGS 102
 Db 87 PENGFGVGGKKKSGKNGSVSFALLSGKEETDNGDKDDEPVISFTGKQASNGK 146
 Oy 103 SNFCV 107
 Db 147 KGFAY 151

RESULT 15

S48423
 hypothetical protein YIL056w - Yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
 C:Accession: S48423
 R:Smith, V.
 submitted to the EMBL Data Library, September 1994
 A:Reference number: S48407
 A:Accession: S48423
 A:Molecule type: DNA
 A:Residues: 1-640 <SMI>
 A:Cross-references: UNIPROT:P40522; UNIPARC:UPI000013B3D4; GB:Z47047; EMBL:Z38060; NID:G
 C:Genetics:
 A:Gene: MIPS:YIL056w
 A:Cross-references: SGD:S0001318
 A:Map position: 91

Query Match 14.4%; Score 80; DB 2; Length 640;
 Best Local Similarity 26.4%; Pred. No. 14;
 Matches 28; Conservative 21; Mismatches 37; Indels 20; Gaps 4;

Oy 15 ELQAKEIEDAEKYSFMAVTYKAPKKQIQFADDM---OEFTKFP-----KTGR 61
 Db 51 QLSQYKASEQDQNTKQIATITLT-----EFGYPVSCSEFEKLVTAAYQVRRNRKRSK 105
 Oy 62 SLRSISQSTDSYSASAYTSSDDEVSPREKQOTNSK--GSSNF 105
 Db 106 RYALSIANGSGGNVNNSSISNSTSDDEISPSIYQRSNDFLPSSNY 151

Search completed: September 6, 2006, 19:30:46
 Job time: 9.29348 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:15:48 ; Search time 56.3152 Seconds
(without alignments)
1806.825 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_110
Perfect score: 555
Sequence: 1 MSMDAMFLPVGEBELKQAK.....PREKQNTSKSSNFCVNI 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	100.0	530	Q96PK4_HUMAN	Q96PK4 homo sapien
2	555	100.0	530	Q80SW1_MOUSE	Q80SW1 mus musculu
3	555	100.0	599	Q27A06_HUMAN	Q27A06 homo sapien
4	555	100.0	607	Q502W8_HUMAN	Q502W8 homo sapien
5	555	100.0	623	Q6P171_HUMAN	Q6P171 homo sapien
6	488	87.9	540	Q5F3Q3_CHICK	Q5F3Q3 gallus gall
7	401	72.3	500	Q48H65_HUMAN	Q48H65 homo sapien
8	355.5	64.1	520	Q661P1_XENLA	Q661P1 xenopus lae
9	353	59.4	505	Q2NKH8_HUMAN	Q2NKH8 homo sapien
10	329.5	53.6	554	Q49S42_BRARE	Q49S42 brachydantio
11	329	59.3	611	Q48H42_HUMAN	Q48H42 homo sapien
12	327	58.9	613	Q68FL3_MOUSE	Q68FL3 mus musculu
13	322.5	58.1	588	Q5BL43_XENTR	Q5BL43 xenopus tro
14	322	58.0	484	Q9UG84_HUMAN	Q9UG84 homo sapien
15	317	57.1	512	Q7T2B5_BRARE	Q7T2B5 brachydantio
16	316	56.9	483	Q5VSM0_HUMAN	Q5VSM0 homo sapien
17	314.5	56.7	588	Q68EX1_XENLA	Q68EX1 xenopus lae
18	309	55.7	591	Q8B1H1_MOUSE	Q8B1H1 mus musculu
19	309	55.7	591	Q6PC06_BRARE	Q6PC06 brachydantio
20	307	55.3	500	Q5R889_PONPY	Q5R889 pongo pygma
21	304	54.8	500	Q49S41_BRARE	Q49S41 brachydantio
22	303	54.6	530	Q6ZNS6_HUMAN	Q6ZNS6 homo sapien
23	299	53.9	491	Q4RXQ1_TESTG	Q4RXQ1 tetraodon n
24	290	52.3	491	Q4RHJ7_TESTG	Q4RHJ7 tetraodon n
25	286	51.5	585	Q4RVT5_TESTG	Q4RVT5 tetraodon n
26	284	51.2	583	Q6AZU3_XENLA	Q6AZU3 xenopus lae
27	193.5	34.6	499	Q4S7H8_TESTG	Q4S7H8 tetraodon n
28	169.5	30.5	193	Q3TMT7_MOUSE	Q3TMT7 mus musculu
29	157.5	28.4	521	Q6NR07_DROME	Q6NR07 drosophila
30	157.5	28.4	521	Q9VZX9_DROME	Q9VZX9 drosophila
31	151	27.2	478	Q80TQ9_MOUSE	Q80TQ9 mus musculu

ALIGNMENTS

RESULT 1	ID	Q96PK4_HUMAN	PRELIMINARY; PRT; 530 AA.
AC	Q96PK4		
DT	01-DEC-2001	integrated into UniProtKB/TrEMBL.	
DT	01-DEC-2001	sequence version 1.	
DT	07-MAR-2006	entry version 25.	
DE	Adenosylhomocysteinease (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-homocysteine hydrolase).		
GN	Name=AHCYL1; ORFNames=RP11-180N18.1-001;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	MEDLINE=21901265; PubMed=11904675; DOI=10.1007/s00251-001-0402-z; Dekker J.W., Budhia S., Angel N.Z., Cooper B.D., Clark G.J., Hart D.N., Kato M., "Identification of an S-adenosylhomocysteine hydrolase-like transcript induced during dendritic cell differentiation."; Immunogenetics 53:993-1001 (2002).		
RL	[2]		
RN	NUCLEOTIDE SEQUENCE.		
RP	Martin S., Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.		
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-homocysteine + adenosine.		
CC	-1- COFACTOR: NAD (By similarity).		
CC	-1- PATHWAY: Activated methyl cycle.		
CC	-1- SIMILARITY: Belongs to the adenosylhomocysteinease family.		
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NonDerivs license		
CC	EMBL; AF315687; AA26869.1; mRNA.		
DR	EMBL; AL772411; CAH70965.1; Genomic DNA.		
DR	HSSP; P10760; 1B3R.		
DR	Ensembl; ENSG00000168710; Homo sapiens.		
DR	GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	GO; GO:0006730; P:one-carbon compound metabolism; IEA.		
DR	InterPro; IPR000043; Ad_hcy_hydrolase.		
DR	InterPro; IPR013321; Arc_fbn_hlx_hlx.		
DR	PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.		
DR	Pfam; PF05221; AdoHcyase; 1.		
DR	Pfam; PF00670; AdoHcyase_NAD; 1.		
DR	TIGRFAMs; TIGR00936; ahcy_1.		
DR	PROSITE; PS00738; ADOHCYASE_1; 1.		
DR	PROSITE; PS00739; ADOHCYASE_2; 1.		
KW	Hydrolase; NAD; One-carbon metabolism.		
SO	SEQUENCE 530 AA; 58951 MW; 974D23361A245D04 CRC64;		

32	104	18.7	492	1	SAHH2_DROME	P50245 drosophila
33	104	18.7	504	2	Q7KSG0_DROME	Q7KSG0 drosophila
34	102.5	18.5	522	2	Q5DH82_SCHJA	Q5DH82 schistosoma
35	97	17.5	1365	2	Q7PZ88_ANOGA	Q7PZ88 anopheles g
36	92	16.8	805	2	Q7RZM4_NEUCR	Q7RZM4 neurospora
37	92	16.6	679	2	Q95XW8_CAEEL	Q95XW8 caenorhabdi
38	90	16.2	651	2	Q86B18_DICDI	Q86B18 dictyosteli
39	90	16.2	680	2	Q92033_ANOPU	Q92033 anolis pulc
40	89	16.0	600	2	Q90237_ANOPU	Q90237 anolis pulc
41	88.5	15.9	623	2	Q7RB34_PLAYO	Q7RB34 plasmodium
42	88	15.9	447	2	Q6BY19_DEBHA	Q6BY19 debaryomyce
43	88	15.9	557	2	Q6K110_MYCWO	Q6K110 mycoplasma
44	88	15.9	1266	2	Q80TU6_MOUSE	Q80TU6 mus musculu
45	87.5	15.8	806	2	Q6FSW1_CANGA	Q6FSW1 candida gla

```

Query Match      100.0%; Score 555; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.3e-39;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMP;PGVGEELKQAKEIEDAEKYSFMAVTTKAPKKQIQFADDMQEFTEFPKTKGR 60
DB 1 MSMPDAMP;PGVGEELKQAKEIEDAEKYSFMAVTTKAPKKQIQFADDMQEFTEFPKTKGR 60

QY 61 RLSRSISQSSSTDYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNI 110
DB 61 RLSRSISQSSSTDYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNI 110

RESULT 2
Q80SW1 MOUSE PRELIMINARY; PRT; 530 AA.
AC Q80SW1;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-MAR-2006, entry version 26.
DE S-adenosylhomocysteine hydrolase-like 1 (IP3R binding protein released
DE with inositol 1,4,5-trisphosphate) (S-adenosylhomocysteine hydrolase-
DE like protein).
GN Name=AHCYL1; Synonyms=Irlt1;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II; TISSUE=Mammary tumor metastasized to lung.
RC MMTV-LTR/Whit model. Expression driven by an MMTV-LTR enhancer.;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munz D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Czech II; TISSUE=Mammary tumor metastasized to lung.
RC MMTV-LTR/Whit model. Expression driven by an MMTV-LTR enhancer.;
RA NIH MGC Project;
RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
[3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Cerebellum;
RA MEDLINE=22526701; PubMed=12525476; DOI=10.1074/jbc.M210119200;
RA Ando H., Mizutani A., Matsunaga T., Mikoshiba K.;
RA "IRBIT, a novel inositol 1,4,5-trisphosphate (IP3) receptor-binding
RA protein," is released from the IP3 receptor upon IP3 binding to the
RA receptor.";
RA J. Biol. Chem. 278:10602-10612(2003).
[4]
RN NUCLEOTIDE SEQUENCE.
RA MEDLINE=21901265; PubMed=11904675; DOI=10.1007/s00251-001-0402-z;
RA Dekker J.W., Budhia S., Angel N.Z., Cooper B.J., Clark G.J.,

```

```

RA Hart D.N., Kato M.;
RT Identification of an S-adenosylhomocysteine hydrolase-like transcript
RT induced during dendritic cell differentiation.;
RL Immunogenetics 53:993-1001(2002).
CC -1 MISCELLANEOUS; The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
CC -1 CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
CC homocysteine + adenosine.
CC -1 COFACTOR: NAD (By similarity).
CC -1 PATHWAY: Activated methyl cycle.
CC -1 SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NoDerivs license
CC
DE EMBL; BC018218; AAH18218.2; -, mRNA.
DE EMBL; AB092504; BAC65166.1; -, mRNA.
DE EMBL; BK000547; DAA00059.1; -, mRNA.
DE HSSP; P10760; 1B3R.
DE Ensemble1; ENSMUSG0000027893; Mus musculus.
DR MGI; MGI:2385184; AHCYL1.
DR GO; GO:0004013; F:adenosylhomocysteinease activity; RCA.
DR GO; GO:0016787; F:hydrolase activity; RCA.
DR GO; GO:0006730; P:one-carbon compound metabolism; RCA.
DR InterPro; IPR000043; Ad_hcy_hydrolase.
DR InterPro; IPR013321; Arc_rbn_hlx_hlx.
DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase_NAD; 1.
DR TIGRFAMs; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADOHCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
SQ SEQUENCE 530 AA; 58951 MW; 974D23361A245D04 CRC64;

Query Match      100.0%; Score 555; DB 2; Length 530;
Best Local Similarity 100.0%; Pred. No. 2.3e-39;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMP;PGVGEELKQAKEIEDAEKYSFMAVTTKAPKKQIQFADDMQEFTEFPKTKGR 60
DB 1 MSMPDAMP;PGVGEELKQAKEIEDAEKYSFMAVTTKAPKKQIQFADDMQEFTEFPKTKGR 60

QY 61 RLSRSISQSSSTDYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNI 110
DB 61 RLSRSISQSSSTDYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNI 110

RESULT 3
Q2TAJ6 HUMAN PRELIMINARY; PRT; 599 AA.
AC Q2TAJ6;
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE AHCYL1 protein (Fragment).
GN Name=AHCYL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

```

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RG NIH MGC Project;
 CC Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DR EMBL: BC110896; AAL10897.1; -; mRNA.
 DR Hydroxylase; NAD; One-carbon metabolism.
 FT NON TER 1
 SO SEQUENCE 599 AA; 65700 MW; C85BAEB1950CEAAB CRC64;
 Query Match 100.0%; Score 555; DB 2; Length 599;
 Best Local Similarity 100.0%; Pred. No. 2; 6e-39;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMPAMPPLPGVGEELKQAKETEDAEKISFPAATVTKAPKKQIQFADDMQEFKPTKTR 60
 DB 70 MSMPAMPPLPGVGEELKQAKETEDAEKISFPAATVTKAPKKQIQFADDMQEFKPTKTR 129
 QY 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCVXNI 110
 DB 130 RLSRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCVXNI 179
 RESULT 4
 ID 0502W8 HUMAN PRELIMINARY; PRT; 607 AA.
 AC 0502W8;
 DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, sequence version 1.
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN (2)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Peripheral Nervous System;
 RG NIH MGC Project;
 CC Submitted (May-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC -----
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC -----
 DR EMBL: BC095476; AAH95476.1; -; mRNA.
 DR Ensemble; ENSG00000168710; Homo sapiens.
 DR GO; GO:004013; F:adenosylhomocysteine activity; IEA.
 DR GO; GO:0046787; F:hydroxylase activity; IEA.
 DR GO; GO:006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad_hcy_hydroxylase.
 DR InterPro; IPR013321; Arc_rtn_hlx_hlx.
 DR InterPro; IPR011128; Cytochrome_P450.
 DR PANTHER; PTHR11784; Ad_hcy_hydroxylase; 1.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF00670; AdoHcyase_NAD; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; UNKNOWN_1.
 DR PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
 DR Hydroxylase; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON TER 1
 SO SEQUENCE 607 AA; 66683 MW; 349412833E2D5911 CRC64;
 Query Match 100.0%; Score 555; DB 2; Length 607;
 Best Local Similarity 100.0%; Pred. No. 2; 7e-35;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSMPAMPPLPGVGEELKQAKETEDAEKISFPAATVTKAPKKQIQFADDMQEFKPTKTR 60
 DB 78 MSMPAMPPLPGVGEELKQAKETEDAEKISFPAATVTKAPKKQIQFADDMQEFKPTKTR 137
 QY 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCVXNI 110
 DB 138 RLSRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCVXNI 187
 RESULT 5
 ID 06P171 HUMAN PRELIMINARY; PRT; 623 AA.
 AC 06P171;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye.
 MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.P., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pabby J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakesley A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzyzanski M.I., Skalska U., Smalins D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RA Strausberg R.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: BC065254; AAH65254.1; -; mRNA.
 CC HSSP: P10760; I33R.
 DR Ensemble: ENSG00000168710; Homo sapiens.
 DR GO: GO:0004013; P:adenosylhomocysteine activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR InterPro: IPR013321; Arc_rhn_hlx_hlx.
 DR InterPro: IPR001128; Cytochrome P450.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase_NAD; 1.
 DR TIGRFAMs: TIGR00936; ahcy; 1.
 DR PROSITE: PS00738; AdoHcyase_1; 1.
 DR PROSITE: PS00739; AdoHcyase_2; 1.
 DR PROSITE: PS00086; CYTOCHROME_P450; UNKNOWN_1.
 KW Hydrolase; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON_TER
 FT 1
 SQ SEQUENCE 623 AA; 68648 MW; B0A40ED58BAF3F23 CRC64;

Query Match 100.0%; Score 555; DB 2; Length 623;
 Best Local Similarity 100.0%; Pred. No. 2.8e-39;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSNPDMPLPGVGEELKQAEIEDAEKYSFMATVTKAPKKQIQFADMDQEFTEPPTKTR 60
 DB 94 MSNPDMPLPGVGEELKQAEIEDAEKYSFMATVTKAPKKQIQFADMDQEFTEPPTKTR 153
 QY 61 RSLRSISQSTDSYSSAASYTSSDDEVPREKQOTNSKSSNFCVKNI 110
 DB 154 RSLRSISQSTDSYSSAASYTSSDDEVPREKQOTNSKSSNFCVKNI 203

RESULT 6
 OSF303_CHICK PRELIMINARY; PRT; 540 AA.
 AC OSF303;
 RT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 PT 07-FEB-2006, entry version 6.

DE Hypothetical protein.
 GN ORFNames=RCMB04_10b17;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
 RA Fiedler P., Kuter S., Biagodatski A., Kostovska D., Kotter M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.,
 RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
 RT gene function analysis.";
 RL Genome Biol. 6:R6-R6(2005).
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL: AJ851597; CAH65231.1; -; mRNA.
 DR GO: GO:0004013; P:adenosylhomocysteine activity; IEA.
 DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR InterPro: IPR013321; Arc_rhn_hlx_hlx.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase_NAD; 1.
 DR PROSITE: PS00738; AdoHcyase_1; 1.
 DR PROSITE: PS00739; AdoHcyase_2; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 540 AA; 59231 MW; 66E479BFA2368F92 CRC64;

Query Match 87.9%; Score 488; DB 2; Length 540;
 Best Local Similarity 90.0%; Pred. No. 1.4e-33;
 Matches 99; Conservative 3; Mismatches 4; Indels 4; Gaps 1;

QY 1 MSNPDMPLPGVGEELKQAEIEDAEKYSFMATVTKAPKKQIQFADMDQEFTEPPTKTR 60
 DB 1 MSNPDMPLPGVGEELKQAEIEDAEKYSFMATVTKAPKKQIQFADMDQEFTEPPTKTR 56
 QY 61 RSLRSISQSTDSYSSAASYTSSDDEVPREKQOTNSKSSNFCVKNI 110
 DB 57 RSLRSISQSTDSYSSAASYTSSDDEVPREKQOTNSKSSNFCVKNI 106

RESULT 7
 SAH2_HUMAN
 ID SAH2_HUMAN STANDARD; PRT; 500 AA.
 AC Q43865;
 DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
 DT 01-JUN-1998, entry version 1.
 DT 07-MAR-2006, entry version 44.
 DE Putative adenosylhomocysteine 2 (EC 3.3.1.1) (S-adenosyl-L-
 DE homocysteine hydrolase) (AdoHcyase).
 GN Name=AHCYL1; Synonyms=XHYKONA;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA].
 RC TISSUE=Skin;
 RA Volpe J.P.G., McDowell M., Jostes R.F., Afzal V., Sadinski W.,
 RA Trask B.J., Legeza R., Cleaver J.E.,
 RT "Complementation of chromosomal instability in the xeroderma
 RT pigmentosum variant by a gene on human chromosome 1 with homology to
 RT S-adenosyl homocysteine hydrolase.";
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=colon, and placenta;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COPACITOR: Binds 1 NAD per subunit (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs license
 CC -----
 CC EMBL: U82761; AAC01960.1; -; mRNA.
 DR EMBL: BC007576; AAH07576.1; -; mRNA.
 DR EMBL: BC010681; AAH10681.1; -; mRNA.
 DR EMBL: BC016942; AAH16942.1; -; mRNA.
 DR HSSP: P10760; 1B3R.
 DR Ensembl: ENSG00000168710; Homo sapiens.
 DR HGNC: HGNC:344; AHCYL1.
 DR MIM: 607826; gene.
 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR InterPro: IPR013321; Arg_rbm_hlx_hlx.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase; 1.
 DR TIGRFAMs: TIGR00936; ahcy; 1.
 DR PROSITE: PS00738; ADOHCYASE_1; 1.
 DR PROSITE: PS00739; ADOHCYASE_2; 1.
 DR HydroLase; NAD: One-carbon metabolism.
 KW CHAIN 1 500
 FT Putative adenosylhomocysteine 2.
 FT REGION 251 418 /FTid=PRO-0000116908.
 FT BINDING 125 125 NAD binding (By similarity).
 FT BINDING 199 199 Substrate (By similarity).
 FT BINDING 224 224 Substrate (By similarity).
 FT BINDING 254 254 Substrate (By similarity).
 FT BINDING 258 258 Substrate (By similarity).
 SQ SEQUENCE 500 AA; 55628 MW; FDEMBFC70044B9DA CRC64;
 Query Match 72.3%; Score 401; DB 1; Length 500;
 Best Local Similarity 100.0%; Pred. No. 4.1e-26;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID 0661P1_XENLA PRELIMINARY; PRT; 520 AA.
 AC 0661P1;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE MG66404 protein.
 GN Name=MG66404;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_Taxid=83355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strassberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RA "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RT Dev. Dyn. 225:384-391(2002).
 RL [2]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strassberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL [3]
 RN NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RX Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 RA Klein S., Gerhard D.S.;
 RL Submitter (Aug-2004) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs license
 CC -----
 CC EMBL: BC081269; AAH81269.1; -; mRNA.
 DR GO: GO:0004013; F:adenosylhomocysteine activity; IEA.
 DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase; 1.
 DR TIGRFAMs: TIGR00936; ahcy; 1.
 DR PROSITE: PS00738; ADOHCYASE_1; 1.
 DR PROSITE: PS00739; ADOHCYASE_2; 1.
 SQ SEQUENCE 520 AA; 57839 MW; C73583CF180234C3 CRC64;
 Query Match 64.1%; Score 355.5; DB 2; Length 520;
 Best Local Similarity 69.1%; Pred. No. 3.6e-22;
 Matches 76; Conservative 9; Mismatches 14; Indels 11; Gaps 2;

RESULT 8
 Q661P1_XENLA
 1 MSMPAMPPLPGVGBELKQAKIEIDAEKYSFMATYTKAPKQIQFADDDQEFKFPRTKGR 60
 1 MSLPEAV-----TTDEPAAAEKFLFMAVPVSKTPKK-IQFADDDQEFKFPRTKGR 49

```

QY 61 RSISRISQSTSDSYSSAASYTSSDDEVSPREKQOTNSKGSNFCVKNI 110
DB 50 RSLRSISQSTSDSYSSAASYTSSDDEVSPREKQOTNSKGSNFCVKNI 99

RESULT 9
Q2NMK8 HUMAN PRELIMINARY; PRT; 505 AA.
ID Q2NMK8 HUMAN
AC Q2NMK8;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE AHCIYL1 protein (Fragment).
GN Name=AHCIYL1;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan A.C., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stacieleto M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.U., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kerteman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
RA Butlerfield Y.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,
RA Generech A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: BC11563; A111564.1; -, mRNA.
FT NON_TER 1 1
SQ SEQUENCE 505 AA; 56469 MW; 0231B614A22D5662 CRC64;

Query Match 63.6%; Score 353; DB 2; Length 505;
Best Local Similarity 98.6%; Pred. No. 5,7e-22;
Matches 70; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 40 KQIQPADDNQEFKPKTKTRSLRSISQSTSDSYSSAASYTSSDDEVSPREKQOTNS 99
DB 15 QOIQPADDNQEFKPKTKTRSLRSISQSTSDSYSSAASYTSSDDEVSPREKQOTNS 74

QY 100 KGSNFCVKNI 110
DB 75 KGSNFCVKNI 85

RESULT 10
Q49S42 BRARE PRELIMINARY; PRT; 554 AA.
ID Q49S42 BRARE

```

```

AC Q49S42;
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DB 07-FEB-2006, entry version 2.
DE S-adenosylhomocysteine hydrolase-like protein variant 1.
GN Name=ahcyl1;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN NUCLEOTIDE SEQUENCE.
RP Cooper B.J., Key B., Carter A., Angel N.Z., Jackson A., Hart D.N.J.,
RA Kato M.;
RA "Ectopic expression of adenosylhomocysteine hydrolase-like protein 1
RT (AHCIYL1) causes dorsoalization of zebrafish embryos: Zebrafish AHCIYL1
RT cloning, gene structure and function.";
RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR EMBL: AY611473; AAU20792.1; -, mRNA.
DR ZFIN: ZDB-GENE-021206-7; ahcyl1.
DR GO: GO:0004013; P:adenosylhomocysteine activity; IEA.
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro: IPR000043; Ad_hcy_hydrolase.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF00670; AdoHcyase; NMD; 1.
DR TIGRfam: TIGR00936; ahcy; 1.
DR PROSITE: PS00738; ADHCYASE_1; 1.
DR PROSITE: PS00739; ADHCYASE_2; UNKNOWN_1.
DR Hydrolase.
KW SEQUENCE 554 AA; 61406 MW; 4EE5F03B1D238BA36 CRC64;

Query Match 59.4%; Score 329.5; DB 2; Length 554;
Best Local Similarity 64.1%; Pred. No. 6,7e-20;
Matches 75; Conservative 6; Mismatches 13; Indels 23; Gaps 3;

QY 17 KOAKETED-AEYKS-----FMATVTKPKQIQPFA--DMQEFK 53
DB 18 KPFKESENVAEKXSMATRKISDVMMNGELSAFAVPTHTSVKKICPANEDEKQEFK 77

QY 54 FPKTKGRSLRSISQSTSDSYSSAASYTSSDDEVSPREKQOTNSKGSNFCVKNI 110
DB 78 FPKTKGRSLRSISQSTSDSYSSAASYTSSDDEVSPREKQOTNSKGSNFCVKNI 134

RESULT 11
SAH33 HUMAN STANDARD; PRT; 611 AA.
ID SAH33 HUMAN
AC Q96HN2; O94917;
DT 11-JUL-2002, integrated into UniProtKB/Swiss-Prot.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 26.
DE Putative adenosylhomocysteine 3 (EC 3.3.1.1) (S-adenosyl-L-
DE homocysteine hydrolase) (AdoHcyase).
GN Name=KIA0828;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RP TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485; DOI=10.1093/dnares/5.6.355;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code

```

for large proteins in vitro.":
 RL DNA Res. 5:355-364(1998).
 RN [12]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RX TISSUE=Lung; and Uterus;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.":
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs license
 CC
 CC EMBL AB020635, BAA74851.1; ALT INIT; mRNA.
 CC EMBL BC008349, AAH08349.1; -, mRNA.
 CC EMBL BC024325, AAH24325.1; -, mRNA.
 CC HSP, F23526, 1L14.
 CC Ensembl: ENSG00000158467, Homo sapiens.
 CC InterPro: IPR000043; Ad_hcy_hydrolase.
 CC PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 CC Pfam: PF05221; AdoHcyase; 1.
 CC Pfam: PF00670; AdoHcyase; 1.
 CC TIGRFAMs: TIGR00936; hncf; 1.
 CC PROSITE: PS00738; ADOHCYASE_1; 1.
 CC PROSITE: PS00739; ADOHCYASE_2; 1.
 CC KEGG: hncf; One-carbon metabolism.
 CC CHAIN 1 611
 FT REGION 362 529 /Ptm-PRO-0000116909.
 FT BINDING 236 236 NAD binding (By similarity).
 FT BINDING 310 310 Substrate (By similarity).
 FT BINDING 335 335 Substrate (By similarity).
 FT BINDING 365 365 Substrate (By similarity).
 FT BINDING 369 369 Substrate (By similarity).
 FT CONFLICT 122 122 Missing (in Ref. 1).
 SQ SEQUENCE 611 AA; 66721 MW; A76B1275FC0D891D CRC64;
 Query Match 59.3%; Score 329; DB 1; Length 611;
 Best Local Similarity 57.3%; Pred. No. 8.3e-20; Indels 28; Gaps 3;
 Matches 75; Conservative 11; Mismatches 17;
 Db 8 PUPGVE-----ELKQAKELIEDAKY-----SFWATYTKAP--K 39
 61 PVPFGSGPRAALSPAGKVRQASAMKSRDPRHNOHRHDEGALVSPGVTYTPK 120
 40 KQIQPADDMOETKPTTKGRSLSSISQSSDTSYSSAASTTDSDDVSPREKQNTS 99
 121 KQIQPADKQEFNKPRTKIGRSLSSISQSSDTSYSSAASTTDSDDVSPREKQNTS 180
 100 KGSNFCVANI 110
 |||:|||||

Db 181 KGSDFCVANI 191
 RESULT 12
 ID 068FL4 MOUSE PRELIMINARY; PRT; 613 AA.
 AC 068FL4;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE RIKEN CDNA 4631427C17.
 GN Name=4631427C17Rik;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain; STRAIN=C57BL/6;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.":
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RC Director MGC Project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- CORFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NoDerivs license
 CC
 CC EMBL BC079660, AAH79660.1; -, mRNA.
 CC Ensembl: ENSMUSG00000029772; Mus musculus.
 CC MGI: MGI:1921590; 4631427C17Rik.
 CC GO: GO:0004013; F:adenosylhomocysteine activity; IEA.
 CC GO: GO:0016787; F:hydrolase activity; IEA.
 CC GO: GO:0006730; P:one-carbon compound metabolism; IEA.
 CC InterPro: IPR000043; Ad_hcy_hydrolase.
 CC PANTHER: PTHR11784; AdoHcyase; 1.
 CC Pfam: PF05221; AdoHcyase; 1.
 CC Pfam: PF00670; AdoHcyase; 1.
 CC TIGRFAMs: TIGR00936; hncf; 1.
 CC PROSITE: PS00738; ADOHCYASE_1; 1.
 CC PROSITE: PS00739; ADOHCYASE_2; 1.
 CC KEGG: hncf; One-carbon metabolism.
 CC CHAIN 613 AA; 66899 MW; 4413DBF1F4825860 CRC64;
 SQ SEQUENCE 613 AA; 66899 MW; 4413DBF1F4825860 CRC64;
 Query Match 58.9%; Score 327; DB 2; Length 613;
 Best Local Similarity 57.3%; Pred. No. 1.2e-19;

Matches 75; Conservative 10; Mismatches 18; Indels 28; Gaps 3;

QY 8 PLPGVGE-----ELKQAKEIEDAEKY-----SFMAVTYKAP--K 39
 DB 63 PAPPGSGPTNALSPAGKVPQASAMKRSDDPHQHQRHBDGALVSPDGTVAFTVK 122
 QY 40 KQIQPADDMQFTFPPTKGRSLRSISQSTSTSYSSAASYTSSDDEVSPPREKQNTS 99
 DB 123 KQIQPADDMQFTFPPTKGRSLRSISQSTSTSYSSAASYTSSDDEVSPPREKQNTS 182
 QY 100 KGSSENFVCYKNI 110
 DB 183 KGSSENFVCYKNI 193

RESULT 13
 05BL43_XENTR PRELIMINARY; PRT; 588 AA.

AC 05BL43;
 DT 12-APR-2005, integrated into UniProtKB/TrEMBL.
 DT 12-APR-2005, sequence version 1.
 DE 07-FEB-2006, entry version 8.
 DE S-adenosylhomocysteine hydrolase-like 1.
 GN Name-acyl-prov;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus; Silurana.
 MX NCBI_Taxid=8364;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 MDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Collins E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Spletten M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidl T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License

CC EMBL; BC090609; AA090609.1; -; mRNA.
 DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
 DR GO; GO:0016787; P:one-carbon compound metabolism; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad_hcy_hydrolase.
 DR Pfam; PF05221; Adhcyase; 1.
 DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam; PF05221; Adhcyase; 1.
 DR TIGRfam; TIGR00936; ahcy; 1.
 DR TIGRfam; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; UNKNOWN_1.
 DR PROSITE; PS00738; ADOHCYASE_1; UNKNOWN_1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.

KW Hydrolase.
 SQ SEQUENCE 588 AA; 64721 MW; 2CBAD9A46134581C CRC64;

Query Match 58.1%; Score 322.5; DB 2; Length 588;
 Best Local Similarity 59.3%; Pred. No. 2.9e-19;
 Matches 73; Conservative 12; Mismatches 21; Indels 17; Gaps 3;

QY 4 PDAMPPLGVGEELKQA-----KEIEDAEKYSFMAVTYKAPK--KQIQPAD 47
 DB 47 PDNSPPLALSGPTKGPASAMKRSDDPTQRPKDGDD-FAQSPGAVSAPFTVKKIQPADQ 105
 QY 48 MOEFKPTKTKGRSLRSISQSTSTSYSSAASYTSSDDEVSPPREKQNTS 107
 DB 106 KREPNKRPFTKGRSLRSISQSTSTSYSSAASYTSSDDEVSPPREKQNTS 165

QY 108 KNI 110
 DB 166 KNI 168

RESULT 14
 09UG84_HUMAN PRELIMINARY; PRT; 484 AA.

AC 09UG84;
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 2.
 DT 07-FEB-2006, entry version 23.
 DE Adenosylhomocysteine hydrolase (EC 3.3.1.1) (Adhcyase) (S-adenosyl-L-
 DE homocysteine hydrolase) (Fragment).
 GN Name=DKFPZ564A1523;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
 OC Homo.
 MX NCBI_Taxid=9606;
 RX [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Brain;
 RA The German cDNA Consortium;
 RA Wambut R., Heubner D., Mewes H.W., Weil B., Amid C., Oeinger A.,
 RA Fobio G., Han M., Wiemann S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
 CC homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License

CC EMBL; AL049954; CAB43223.2; -; mRNA.
 DR PIR; T08681; T08681.
 DR Ensembl; ENSG00000168710; Homo sapiens.
 DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
 DR GO; GO:0016787; P:hydrolyase activity; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad_hcy_hydrolase.
 DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam; PF05221; Adhcyase; 1.
 DR Pfam; PF06670; Adhcyase; 1.
 DR TIGRfam; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 DR HYDROLASE; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON TER 1
 SQ SEQUENCE 484 AA; 53869 MW; 8A5SEF564FEB7EID CRC64;

Query Match 58.0%; Score 322; DB 2; Length 484;
 Best Local Similarity 100.0%; Pred. No. 2.6e-19;
 Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 DMQEFKPTKTKGRSLRSISQSTSTSYSSAASYTSSDDEVSPPREKQNTS 106

Db 1 DMQEFKPTKGRSLRSISQSSSTDYSSAASTYDSSDDEVSPREKQOTNSKSSNFC 60
QY 107 VKNI 110
61 VKNI 64

RESULT 15

ID Q7T2B5_BRARE PRELIMINARY; PRT; 512 AA.
AC Q7T2B5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE S-adenosylhomocysteine hydrolase-like 1.
GN Name=ahcy11;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney.

MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney.
RA Strausberg R.L.
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs License
CC
EMBL: BC054614; AAHS4614.1; -, mRNA.
DR HSSP; P10760; IB3R.
DR ZFIN; ZDB-GENE-021206-7; ahcy11.
DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR000043; Ad_hcy_hydrolase.
DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam; PF05221; AdoHcyase; 1.
DR TIGRFAMs; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
DR HydroLase.
SQ SEQUENCE 512 AA; 56776 MW; 3E0A09DFF086683 CRC64;

Query Match - 57.1%; Score 317; DB 2; Length 512;
Best Local Similarity 78.6%; Pred. No. 7.3e-19;

Matches 66; Conservative 5; Mismatches 11; Indels 2; Gaps 1;
QY 29 SPMATVTAKPKKQIOFA--DMQEFKPTKGRSLRSISQSSSTDYSSAASTYDSSD 86
Db 9 AFTAVPTKSVKIOFANQEDKQEFSPPTKGRSLRSISQSSSTDYSSAASTYDSSD 68
QY 87 DEVSPREKQOTNSKSSNFCVKNI 110
Db 69 DETSPREKQVNSKSSDFCVKNI 92

Search completed: September 6, 2006, 19:29:40
Job time : 58.3152 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:30:04; Search time 11 Seconds
(without alignments)
875.306 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_110
Perfect score: 555
Sequence: I MSMNDAMPPLPGVEELKQAK.....PREKQGTNSKSGSNFCVKN1 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /EMC_Celerra_SIDS3/prodata/2/1aa/5.COMB.pap:*
2: /EMC_Celerra_SIDS3/prodata/2/1aa/6.COMB.pap:*
3: /EMC_Celerra_SIDS3/prodata/2/1aa/7.COMB.pap:*
4: /EMC_Celerra_SIDS3/prodata/2/1aa/H.COMB.pap:*
5: /EMC_Celerra_SIDS3/prodata/2/1aa/PCTUS.COMB.pap:*
6: /EMC_Celerra_SIDS3/prodata/2/1aa/RE.COMB.pap:*
7: /EMC_Celerra_SIDS3/prodata/2/1aa/backfl1e1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	401	72.3	500	1	US-08-896-005-1 Sequence 1, Appli
2	104	18.7	504	1	US-08-896-005-3 Sequence 5, Appli
3	86.5	15.6	414	1	US-07-667-2276A-4 Sequence 98, Appli
4	81.5	14.7	542	2	US-09-538-092-289 Sequence 22, Appli
5	79.5	14.3	703	2	US-08-910-925-4 Sequence 21, Appli
6	79	14.2	998	2	US-09-949-016-7757 Sequence 24096, A
7	77.5	14.0	233	2	US-09-270-767-45949 Sequence 17, Appli
8	76	13.7	191	2	US-09-248-796A-15111 Sequence 15, Appli
9	76	13.7	754	2	US-09-976-594-375 Sequence 30, Appli
10	76	13.7	760	2	US-09-949-016-11129 Sequence 1114, Ap
11	75.5	13.6	124	2	US-09-270-767-34893 Sequence 30, Appli
12	75.5	13.6	124	2	US-09-270-767-50110 Sequence 18842, A
13	74.5	13.6	414	2	US-09-248-796A-19046 Sequence 21575, A
14	74.5	13.4	442	2	US-09-248-796A-19805 Sequence 17, Appli
15	74	13.3	800	2	US-09-949-016-7703 Sequence 15, Appli
16	73.5	13.2	1356	3	US-10-114-270-78 Sequence 30, Appli
17	72.5	13.1	208	2	US-09-925-637-52 Sequence 1114, Ap
18	72.5	13.1	288	2	US-10-094-749-2785 Sequence 21785, Ap
19	72.5	13.1	439	2	US-08-860-368B-14 Sequence 24096, A
20	72.5	13.1	441	2	US-09-248-796A-26086 Sequence 26086, A
21	72.5	13.1	984	1	US-08-257-073-3 Sequence 3, Appli
22	72.5	13.1	984	1	US-08-184-008-120 Sequence 120, App
23	72.5	13.1	984	1	US-08-458-356-120 Sequence 120, App
24	72.5	13.1	984	2	US-08-460-736-120 Sequence 120, App
25	72.5	13.1	984	2	US-09-535-370-120 Sequence 120, App
26	72.5	13.1	984	2	US-09-663-667-120 Sequence 120, App

27	72	13.0	828	2	US-09-327-984A-2	Sequence 2, Appli
28	72	13.0	1850	2	US-09-620-093A-5	Sequence 5, Appli
29	72	13.0	3256	2	US-09-919-172-98	Sequence 98, Appli
30	72	13.0	3256	2	US-09-976-594-22	Sequence 22, Appli
31	72	13.0	3256	2	US-09-919-039-21	Sequence 21, Appli
32	71.5	12.9	129	2	US-09-248-796A-24096	Sequence 24096, A
33	71.5	12.9	291	2	US-08-860-368B-17	Sequence 17, Appli
34	71.5	12.9	379	2	US-08-860-368B-15	Sequence 15, Appli
35	71.5	12.9	568	1	US-08-320-558-30	Sequence 30, Appli
36	71.5	12.9	568	2	US-08-545-860D-30	Sequence 30, Appli
37	71.5	12.9	568	2	US-09-538-092-1114	Sequence 1114, Ap
38	71.5	12.9	568	5	PCT-US94-04496-30	Sequence 30, Appli
39	71.5	12.9	792	2	US-09-248-796A-18842	Sequence 18842, A
40	71	12.8	265	2	US-09-248-796A-18842	Sequence 18842, A
41	70.5	12.7	236	2	US-09-248-796A-21575	Sequence 21575, A
42	70.5	12.7	680	2	US-10-094-749-2158	Sequence 2158, Ap
43	70.5	12.7	684	2	US-09-252-991A-28604	Sequence 28604, A
44	70	12.6	177	2	US-09-247-155-164	Sequence 164, App
45	70	12.6	177	2	US-09-903-190-164	Sequence 164, App

ALIGNMENTS

RESULT 1
US-08-896-005-1
; Sequence 1, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purni
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 1174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PR-0337 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 500 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BLADTUT04
; CLONE: 1519044
; US-08-896-005-1
Query Match 72.3%; Score 401; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-38;

```
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 31 MATVTAPKKQIQFADDMQEFKPTKGRSLRSISQSTDSYSSAASYTSDSDVS 90
Db 1 MATVTAPKKQIQFADDMQEFKPTKGRSLRSISQSTDSYSSAASYTSDSDVS 60
Qy 91 PREKQOTNSKSSNFCVKNI 110
Db 61 PREKQOTNSKSSNFCVKNI 80

RESULT 2
US-08-896-005-3
; Sequence 3, Application US/08896005
; Patent No. 5854023
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Lal, Freeel
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/896,005
; FILING DATE: Filed Herewith
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0337 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 504 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 969078
; US-08-896-005-3

Query Match 18.7%; Score 104; DB 1; Length 504;
Best Local Similarity 50.0%; Pred. No. 0.0014;
Matches 24; Conservative 9; Mismatches 13; Indels 2; Gaps 2;
Qy 64 SRSISGSDTDSYSSAASYTSDSDSDE-VSPREKQOTNSKSSNFCVKNI 110
Db 27 ARRFVSTCSFSTC-FTGSSDSEBVSFKDNHQRRNSAGGTDFCVKSI 73

RESULT 3
US-07-667-276A-4
; Sequence 4, Application US/07667276A
; Patent No. 5470971
; GENERAL INFORMATION:
; APPLICANT: Kondo, Keiji

APPLICANT: Inouye, Masayori
; TITLE OF INVENTION: STRESS-INDUCED PROTEINS, GENES CODING
; TITLE OF INVENTION: THEREFOR, TRANSFORMED CELLS OF ORGANISMS, METHODS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Weiser & Associates
; STREET: 230 S. Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/667,276A
; FILING DATE: 11-MAR-1991
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377.5351P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-667-276A-4

Query Match 15.6%; Score 86.5; DB 1; Length 414;
Best Local Similarity 31.4%; Pred. No. 0.12; 39; Indels 15; Gaps 3;
Matches 32; Conservative 16; Mismatches 15; Indels 15; Gaps 3;
Qy 17 KOAKEIEDAEKYSFATVTKAPKKQIQFADDMQEFKPTKGRSLRSISQSTDSYSS 76
Db 18 KOAKE-EKAKAVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 76
Qy 77 -----SAASYTSDSDVSPREKQOT---NSKSSN 104
Db 77 EAETKKEESKSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 118

RESULT 4
US-09-538-092-289
; Sequence 289, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Glot, Iolc
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurataseqFormatter Version 0.9
; SEQ ID NO 289
; LENGTH: 542
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
```

OTHER INFORMATION: Polypeptide Accession Number YG1028C
US-09-538-092-289

Query Match 14.7%; Score 81.5; DB 2; Length 542;
Best Local Similarity 26.7%; Pred. No. 0.67;
Matches 27; Conservative 20; Mismatches 45; Indels 9; Gaps 2;

11 GVEELKQAKELDEAKYFMAVTYKPKQIQFADDMQEFTK-----PFTKGRSL 63
174 GVEENVEEN--TQSQHSHYQAATSTLNQQTSTIASSESTNTPTSTSTSTSS 231

64 SRSISQSTDSYSAASYTSSDDEVS PREKQOTNSKGSN 104
222 TSSSTSSSTSSSTSSSTSSSTSSSTSTSTSTSTSTSTSTSTSTSTSTSTSS 272

RESULT 5
US-08-910-925-4

Sequence 4, Application US/08910925

Patent No. 6162601

GENERAL INFORMATION:

APPLICANT: Bandman, Olga

APPLICANT: Lal, Preeti

APPLICANT: Shah, Purvi

TITLE OF INVENTION: HUMAN PININ SPLICE VARIANT

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/910,925

FILING DATE: Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0365 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 703 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1684843

US-08-910-925-4

Db 571 TSKRSRGARRNTSKSRSSSSSSSSSTSSSSGSSSSSSSSSRSTSSSS 624

RESULT 6
US-09-949-016-7757
Sequence 7757, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO: 7757

LENGTH: 998

TYPE: PRT

ORGANISM: Human

US-09-949-016-7757

Query Match 14.2%; Score 79; DB 2; Length 998;
Best Local Similarity 29.8%; Pred. No. 3.1; Mismatches 48; Indels 8; Gaps 4;
Matches 31; Conservative 17

2 SMPDAPLPVGEEL--KQAKELDEAKYFMAVTYKPKQIQFADDMQEFTKPFTKGR 60
481 TPTQAPPLSREERYRQRLKEBEKK-----SKLDEFTNDPAKELMEYKKI--QKERR 534

61 RSLRSISQSTDSYSAASYTSSDDEVS PREKQOTNSKGSN 104
535 RSFSRSKSPYSGSSY-SRSSYTSKSRSGSTRSRSYRSFSRSH 577

RESULT 7
US-09-270-767-45949
Sequence 45949, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-034

CURRENT APPLICATION NUMBER: US/09/270,767

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 45949

LENGTH: 233

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-45949

Query Match 14.0%; Score 77.5; DB 2; Length 233;
Best Local Similarity 39.2%; Pred. No. 0.61;
Matches 20; Conservative 10; Mismatches 20; Indels 1; Gaps 1;

56 TKTGRSLSRSISQSTDSYSS-AAASYTSSDDEVS PREKQOTNSKGSNF 105
17 TSTGRSKSKTSKQSTSPFANRAPEFCGSKNNISPLGLQTNKSKMDNF 67

RESULT 8
US-09-248-796A-15111
Sequence 15111, Application US/09248796A
Patent No. 6747137

```
/ GENERAL INFORMATION:
/ APPLICANT: Keith Weinstein et al
/ TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
/ FILE REFERENCE: 107196.132
/ CURRENT APPLICATION NUMBER: US/09/248,796A
/ PRIOR FILING DATE: 1999-02-12
/ PRIOR APPLICATION NUMBER: US 60/074,725
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 60/096,409
/ PRIOR FILING DATE: 1998-08-13
/ NUMBER OF SEQ ID NOS: 28208
/ SEQ ID NO 1511
/ LENGTH: 191
/ TYPE: PRT
/ ORGANISM: Candida albicans
US-09-248-796A-15111

Query Match      13.7%; Score 76; DB 2; Length 191;
Best Local Similarity 23.3%; Pred. No. 0.7;
Matches 27; Conservative 25; Mismatches 48; Indels 16; Gaps 5;

Db      2 SMPDAMPLGVGVELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFPTKPTGRSL 56
      32 SLPDSK--PDTPKPSKTSGNTGGDS-----TENKEDLDPLDELOHEKTKTKTKS 84
QY      57 KTGRRSLRSISQSTDSYSAASYTDS--DEVSPREKQOTNSKSSNFCVK 109
      85 KAPKASKPTS-SDADDEPTTTTDTKSDTTEIDIEPQQPQKTEESDNODIPN 139

RESULT 9
US-09-976-594-375
/ Sequence 375, Application US/09976594
/ Patent No. 6673549
/ GENERAL INFORMATION:
/ APPLICANT: Furness, Michael
/ APPLICANT: Buchinder, Jenny
/ TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
/ FILE REFERENCE: PA-0041 US
/ CURRENT APPLICATION NUMBER: US/09/976,594
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/240,409
/ PRIOR FILING DATE: 2000-10-12
/ NUMBER OF SEQ ID NOS: 1143
/ SOFTWARE: PERL Program
/ SEQ ID NO 375
/ LENGTH: 754
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6673549 368791CD1
US-09-976-594-375

Query Match      13.7%; Score 76; DB 2; Length 754;
Best Local Similarity 29.9%; Pred. No. 4.7;
Matches 29; Conservative 14; Mismatches 34; Indels 20; Gaps 4;

QY      13 GELTKAKETIE---DAEKYSF-----MATVTAKPKKQIQFADDMQEFPTKPTGRSL 63
      147 GQEV--VREIENQKTDAAKFAEVRILSCGELIPKSKV-----KEKKRKHS 195
DB      64 SRSISQSTDSYSAASYTDSDEVSPREKQOTNSK 100
      196 SSSSSSSSDSSSDSSSDSSSDSSSSEKSKKKRK 232

RESULT 10
US-09-949-016-11129
/ Sequence 1129, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
```

```
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11129
/ LENGTH: 760
/ TYPE: PRT
/ ORGANISM: Human
US-09-949-016-11129

Query Match      13.7%; Score 76; DB 2; Length 760;
Best Local Similarity 29.9%; Pred. No. 4.7;
Matches 29; Conservative 14; Mismatches 34; Indels 20; Gaps 4;

QY      13 GELTKAKETIE---DAEKYSF-----MATVTAKPKKQIQFADDMQEFPTKPTGRSL 63
      153 GQEV--VREIENQKTDAAKFAEVRILSCGELIPKSKV-----KEKKRKHS 201
DB      64 SRSISQSTDSYSAASYTDSDEVSPREKQOTNSK 100
      202 SSSSSSSSDSSSDSSSDSSSDSSSSEKSKKKRK 238

RESULT 11
US-09-270-767-34893
/ Sequence 34893, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
/ PRIOR FILING DATE: 1999-03-17
/ NUMBER OF SEQ ID NOS: 62517
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 34893
/ LENGTH: 124
/ TYPE: PRT
/ ORGANISM: Drosophila melanogaster
US-09-270-767-34893

Query Match      13.6%; Score 75.5; DB 2; Length 124;
Best Local Similarity 26.2%; Pred. No. 0.44;
Matches 28; Conservative 17; Mismatches 37; Indels 25; Gaps 3;

QY      23 EDAEKYSFMAVTYTK-----APKKQI-----QFADDMQEFPTKPTGRSLRS 66
      67 ISQSTDSYSAASYTDSDEVSPREKQOTNSKSSN 104
      62 SSSSSSSSDSSSDSSSDSSSDSSSDSSSDSSSGSDSDS 108
DB      67 ISQSTDSYSAASYTDSDEVSPREKQOTNSKSSN 104
      62 SSSSSSSSDSSSDSSSDSSSDSSSDSSSDSSSGSDSDS 108

RESULT 12
US-09-270-767-50110
/ Sequence 50110, Application US/09270767
/ Patent No. 6703491
/ GENERAL INFORMATION:
/ APPLICANT: Homburger et al.
/ TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
/ FILE REFERENCE: File Reference: 7326-094
/ CURRENT APPLICATION NUMBER: US/09/270,767
```

```

; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50110
; LENGTH: 124
; TYPE: prt
; ORGANISM: Drosophila melanogaster
US-09-270-767-50110
```

Query Match	13.6%	Score 75.5;	DB 2;	Length 124;
Best Local Similarity	26.2%	Pred. No. 0.44;		
Matches 28; Conservative	17;	Mismatches 37;	Indels 25;	Gaps 3

QY 23 EDKESYFEMATVTK-----APKKOI--OFADDMOEFTEFPKTGRRLSLKS 66
:::|::|
Dd 2 KKKKYVHRSSRTQLSKMSQEKADPKNQVEHSPVASSECKAYRRKKRXTKSSSSSS 61
:
QY 67 ISOSTDSYS-----SAASYTSDSDEEVPREKQCTNMGSGSN 104
:::|::|
Dd 62 SSSTSSDSSSEGGSSSESDSSSSSDDBDEGSSDSSGGGSDDSS 108

```

RESULT 13
US-09-248-796A-19046
; Sequence 19046, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248, 796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074, 725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19046
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-19046

```

```

QY      9  LPGVGELKQ-AKETEDAEKYSFMATVTKAPKQIQAPDDMQEFPKPTKGRSLRSI 67
      ||::||::||::||::||::||::||::||::||::||::||::||::||
Db     97  LPKFSKOLESTIDEVENOEKTS-----KPNSSDSDESYSESSESTDSSESSSD 149

      68  S-----QSTDSYSSAASYTDSDD-----EVSFPEKQDTNSKGSNN 104
      ||::||::||::||::||::||::||::||::||::||::||::||
Db    150  SFSSDSSESSSDSSSSSDSDSDDEBKEDKEAEKDKNDKSDSDSN 195

```

```

RESULT 14
US-09-248-796A-19805
Sequence 19805, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208

```

```

; SEQ ID NO 19805
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19805

```

Query Match	13.4%;	Score 74.5;	DB 2;	Length 442;
Best Local Similarity	33.0%;	Pred. No. 3.3;		
Matches 31; Conservative	11;	Mismatches 31;	Indels 21;	Gaps 6;

```

QY      23  EDEKESFMAATYTKAKKQIOFADDMOEFTEP-----TKGRRLSRIS-----OSST 72
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      193  DVEVSY-FGGSYSTV--SSTPELDD--FFVPPQOPRTHTRKKKHHISIPSPADSSSS 247
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      73  DSY-----SSAASYTSSDDEVSFREKQOQNSK 100
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      248  SSTVFPOLIPSSSSSVTSNGDSFVSPSTTKRKTTK 281
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 15
US-09-949-016-7703
; Sequence 7703, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7703
; LENGTH: 800
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-7703

```

Query Match	13.3%	Score 74;	DB 2;	Length 800;
Best Local Similarity	28.4%;	Pred. No. 8.7;		
Matches	33;	Conservative 18;	Mismatches 51;	Indels 14; Gaps 4.
Qy	4	PDAMPLEGVGEELKQAKEIEDAEKYSPMATVYAPKKQIOFADDMOEFKEPTTKGRSL	63	
		: : : : :	:	
Db	435	PPAKIMMSKEELHSQKKOLEKRLDLVNQNLSRKQOT-SIKTQPSKAIVENVSRISE	492	
		: : : : :	:	
Qy	64	SRSISOGSTYSAA--SYTDSSD-----EVSPEEK-OQTNSKGSSNFCV	107	
		: : : : :	:	
Db	493	SSSSSSSSSSBSSSDSSDSSDSSEMFPKTEVKPMPDSPENKENVKMKMNCI	548	
		: : : : :	:	

Search completed: September 6, 2006, 19:32:23
Job time : 12 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using .sw model

Run on: September 6, 2006, 19:51:10 : Search time 36.587 Seconds
(without alignments)
1392.672 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_110
Perfect score: 555
Sequence: 1 MSMPAMPPLPGVGEELKQAK.....PREKQOTNSKSSNFCVKNI 110

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	555	100.0	239	US-09-925-300-1379	Sequence 1379, Ap
2	555	100.0	530	US-10-876-285-2	Sequence 2, Appl
3	555	100.0	530	US-10-876-285-4	Sequence 4, Appl
4	555	100.0	530	US-10-876-285-6	Sequence 6, Appl
5	555	100.0	530	US-10-876-285-8	Sequence 8, Appl
6	555	100.0	530	US-10-876-285-10	Sequence 1, Appl
7	555	100.0	614	US-09-782-051-2	Sequence 2, Appl
8	555	100.0	614	US-11-110-748-2	Sequence 2, Appl
9	322.5	58.1	455	US-10-450-763-42388	Sequence 42388, A
10	322.5	58.1	619	US-10-756-149-5569	Sequence 5569, Ap
11	320.5	57.7	257	US-10-424-599-21758	Sequence 21758, Ap
12	307	55.3	564	US-10-467-903-1	Sequence 1, Appl
13	157.5	28.4	521	US-11-097-143-2781	Sequence 2781, Ap
14	104	18.7	504	US-11-097-143-41922	Sequence 41922, A
15	87	15.7	2296	US-10-696-909A-46	Sequence 46, Appl
16	86.5	15.6	414	US-11-004-418A-28	Sequence 28, Appl
17	86.5	15.6	414	US-11-089-551A-28	Sequence 28, Appl
18	84.5	15.2	321	US-10-424-599-169465	Sequence 169465, A
19	83.5	15.0	2058	US-10-052-648A-20	Sequence 20, Appl
20	83	15.0	475	US-10-437-963-120425	Sequence 120425, A
21	83	15.0	628	US-10-869-493-22576	Sequence 22576, A
22	83	15.0	2645	US-10-732-923-8232	Sequence 8232, Ap
23	82.5	14.9	333	US-11-097-143-33054	Sequence 33054, A
24	81.5	14.7	428	US-10-451-467A-448	Sequence 448, Appl
25	80.5	14.5	166	US-10-425-115-264771	Sequence 264771, A
26	80.5	14.5	740	US-10-437-963-134499	Sequence 134499, A
27	79.5	14.3	156	US-09-925-301-1154	Sequence 1154, Ap

28	79.5	14.3	176	US-11-097-143-40977	Sequence 40977, A
29	79.5	14.3	2752	US-10-696-909A-44	Sequence 44, Appl
30	79	14.2	948	US-10-308-448-15	Sequence 15, Appl
31	79	14.2	948	US-10-934-998-295	Sequence 295, Appl
32	79	14.2	948	US-10-523-477-14	Sequence 14, Appl
33	79	14.2	1616	US-10-934-998-88	Sequence 88, Appl
34	78.5	14.1	275	US-10-424-599-231467	Sequence 231467, A
35	78	14.1	1067	US-10-732-923-8348	Sequence 8348, Ap
36	78	14.1	1311	US-10-732-923-8756	Sequence 8756, Ap
37	78	14.1	1311	US-10-732-923-8758	Sequence 8758, Ap
38	78	14.1	1311	US-11-097-143-9036	Sequence 9036, Ap
39	78	14.1	1406	US-11-097-143-42681	Sequence 42681, A
40	77.5	14.0	450	US-10-153-668-380	Sequence 380, Appl
41	77.5	14.0	472	US-11-096-568A-29864	Sequence 29864, A
42	77.5	14.0	491	US-11-096-568A-29863	Sequence 29863, A
43	77.5	14.0	537	US-11-097-143-36798	Sequence 36798, A
44	77.5	14.0	648	US-11-097-143-16119	Sequence 16119, A
45	77.5	14.0	651	US-11-096-568A-29862	Sequence 29862, A

ALIGNMENTS

RESULT 1
US-09-925-300-1379
Sequence 1379, Application US/09925300
Patent No. US20020151681A1
GENERAL INFORMATION:
APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben,
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA101
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1379
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (229)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (231)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (234)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1379
Query Match : 100.0%; Score 555; DB 3: Length 239;
Best Local Similarity 100.0%; Pred. No. 4.1e-46;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMATVTKARKKOIQFADMDQEFPTKTKR 60
DB 86 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMATVTKARKKOIQFADMDQEFPTKTKR 145
QY 61 RLSSISIQSSTDSYSSAASYDSSDDEVSPREKQOTNSKSSNFCVKNI 110
DB 146 RLSSISIQSSTDSYSSAASYDSSDDEVSPREKQOTNSKSSNFCVKNI 195
RESULT 2
US-10-876-285-2
Sequence 2, Application US/10876285
Publication No. US20050044582A1

```

; GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 530
; TYPE: PRT
; ORGANISM: human
US-10-876-285-2
```

```
Query Match          100.0%; Score 555; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
DB 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
```

```
QY 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
DB 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
```

```
RESULT 3
US-10-876-285-4
```

```

; Sequence 4, Application US/10876285
; Publication No. US20050044582A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Human
US-10-876-285-4
```

```
Query Match          100.0%; Score 555; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
DB 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
```

```
QY 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
DB 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
```

RESULT 4

```

US-10-876-285-6
; Sequence 6, Application US/10876285
; Publication No. US20050044582A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
US-10-876-285-6
```

```
Query Match          100.0%; Score 555; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
DB 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
```

```
QY 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
DB 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
```

```
RESULT 5
US-10-876-285-8
```

```

; Sequence 8, Application US/10876285
; Publication No. US20050044582A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; PRIOR FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
US-10-876-285-8
```

```
Query Match          100.0%; Score 555; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.1e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
DB 1 MSMPDAMPPLPGVGBELKQAEIEDAEKYSFMATVTKAPKKQIOFADDMQEFTEFTKPTKGR 60
```

```
QY 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
DB 61 RSLSRISQSSTDSYSSAASYTDSDEVS PREKQOTNSKGSNFCVKNI 110
```

RESULT 6

US-10-683-610-1
; Sequence 1, Application US/10683610
; Publication No. US20050181450A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; TITLE OF INVENTION: A novel inositol 1,4,5-trisphosphate (IP3) receptor binding prote
; TITLE OF INVENTION: IP3
; TITLE OF INVENTION: Indicator
; FILE REFERENCE: PH-1852
; CURRENT APPLICATION NUMBER: US/10/683,610
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: JP 2002-299429
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-683-610-1

Query Match 100.0%; Score 555; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSMPDAMP.LPGVGEELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
DB 1 MSMPDAMP.LPGVGEELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
OY 61 RSLRSISQSSSTDSYSSAASYTDSDDDEVSPREKQNTSKSGSNFCVKN 110
DB 61 RSLRSISQSSSTDSYSSAASYTDSDDDEVSPREKQNTSKSGSNFCVKN 110

RESULT 7

US-09-782-051-2
; Sequence 2, Application US/09782051
; Patent No. US20020035078A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
; FILE REFERENCE: 24305 MRB
; CURRENT APPLICATION NUMBER: US/09/782,051
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: PCT/NZ97/00133
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: NZ 299507
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-051-2

Query Match 100.0%; Score 555; DB 3; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSMPDAMP.LPGVGEELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
DB 85 MSMPDAMP.LPGVGEELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 144
OY 61 RSLRSISQSSSTDSYSSAASYTDSDDDEVSPREKQNTSKSGSNFCVKN 110
DB 145 RSLRSISQSSSTDSYSSAASYTDSDDDEVSPREKQNTSKSGSNFCVKN 194

RESULT 8

US-11-110-748-2
; Sequence 2, Application US/11110748
; Publication No. US20050282765A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
; FILE REFERENCE: 24305 MRB
; CURRENT APPLICATION NUMBER: US/11/110,748
; PRIOR FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: PCT/NZ97/00133
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: NZ 299507
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-110-748-2

Query Match 100.0%; Score 555; DB 6; Length 614;
Best Local Similarity 100.0%; Pred. No. 1.4e-47;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSMPDAMP.LPGVGEELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 60
DB 85 MSMPDAMP.LPGVGEELKQAKIEIDAEKYSFMAVTYTKAPKKQIQFADDMQEFKPTKTGR 144
OY 61 RSLRSISQSSSTDSYSSAASYTDSDDDEVSPREKQNTSKSGSNFCVKN 110
DB 145 RSLRSISQSSSTDSYSSAASYTDSDDDEVSPREKQNTSKSGSNFCVKN 194

RESULT 9

US-10-450-763-42388
; Sequence 42388, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseed, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 42388
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens

FEATURE:
NAME/KEY: DOMAIN
LOCATION: (356)..(388)
OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
OTHER INFORMATION: identified by EMATRIX, accession number BL00738F, p-value=7.261e-
OTHER INFORMATION: 29, raw score of 12.23
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (186)..(447)
OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase domain identified by
OTHER INFORMATION: Pfam, accession name Adohcyase, E-value=6.2e-171, Pfam score of
OTHER INFORMATION: 581.3
US-10-450-763-42388

Query Match 58.1%; Score 322.5; DB 5; Length 455;

```
Best Local Similarity 56.2%; Pred. No. 4.1e-24;
Matches 73; Conservative 13; Mismatches 17; Indels 27; Gaps 3;

QY 8 PLPGVGE-----ELKQAKETEDAEKY-----SFMATVTKAPK--K 40
Db 61 PVPGSGSPALALSPAAGKVPQASAMKRSDPHHQHQRHDDGEGALVSPDGTVEAPRTYK 120

QY 41 QIQFADDMQEFPTKPTKGRSLRSRSISQSTDSYSSAASYTDSDEVSPEKQQTNSK 100
Db 121 KIQFADQKQEFNKRPTKIGRSLRSRSISQSTDSYSSAASYTDSDETSPRDKQKNSK 180

QY 101 GSSNFCVKNI 110
Db 181 GSSDFCVKNI 190

RESULT 10
US-10-756-149-5569
; Sequence 5569, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS AND
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5569
; LENGTH: 619
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-756-149-5569

Query Match 58.1%; Score 322.5; DB 5; Length 619;
Best Local Similarity 56.2%; Pred. No. 6.1e-24;
Matches 73; Conservative 13; Mismatches 17; Indels 27; Gaps 3;

QY 8 PLPGVGE-----ELKQAKETEDAEKY-----SFMATVTKAPK--K 40
Db 70 PVPGSGSPALALSPAAGKVPQASAMKRSDPHHQHQRHDDGEGALVSPDGTVEAPRTYK 129

QY 41 QIQFADDMQEFPTKPTKGRSLRSRSISQSTDSYSSAASYTDSDEVSPEKQQTNSK 100
Db 130 KIQFADQKQEFNKRPTKIGRSLRSRSISQSTDSYSSAASYTDSDETSPRDKQKNSK 189

QY 101 GSSNFCVKNI 110
Db 190 GSSDFCVKNI 199

RESULT 11
US-10-424-599-212758
; Sequence 212758, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212758
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
```

```
; NAME/KEY: unsure
; LOCATION: (1)..(257)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_34146C.1.pcp
US-10-424-599-212758

Query Match 57.7%; Score 320.5; DB 4; Length 257;
Best Local Similarity 56.2%; Pred. No. 3.2e-24;
Matches 73; Conservative 12; Mismatches 18; Indels 27; Gaps 3;

QY 8 PLPGVGE-----ELKQAKETEDAEKY-----SFMATVTKAPK--K 40
Db 63 PVPGSGSPALALSPAAGKVPQASAMKRSDPHHQHQRHDDGEGALVSPDGTVEAPRTYK 122

QY 41 QIQFADDMQEFPTKPTKGRSLRSRSISQSTDSYSSAASYTDSDEVSPEKQQTNSK 100
Db 123 KIQFADQKQEFNKRPTKIGRSLRSRSISQSTDSYSSAASYTDSDETSPRDKQKNSK 182

QY 101 GSSNFCVKNI 110
Db 183 GSSDFCVKNI 192

RESULT 12
US-10-467-903-1
; Sequence 1, Application US/10467903
; Publication No. US20040265807A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: SANJAMALA, Madhusudan M.
; APPLICANT: LU, Yan
; APPLICANT: LEE, Ernestine A.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Montique G.
; APPLICANT: LEE, Sally
; APPLICANT: THORNTON, Michael B.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: XU, Yuming
; APPLICANT: TRAN, Dyen K.
; APPLICANT: LAL, Preeti G.
; APPLICANT: LU, Dyang, Aina M.
; APPLICANT: SMARNAKAR, Anita
; APPLICANT: RING, Huijun Z.
; APPLICANT: JONES, Karen A.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PI-0360 USN
; CURRENT APPLICATION NUMBER: US/10/467,903
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: PCT/US02/03814
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/268,113
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/269,215
; PRIOR FILING DATE: 2001-02-15
; PRIOR APPLICATION NUMBER: US 60/272,271
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: US 60/274,091
; PRIOR FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 60/274,423
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 60/278,480
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,479
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 564
```

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7484737CD1
US-10-467-903-1

```

```

Query Match      55.3%; Score 307; DB 5; Length 564;
Best Local Similarity 75.0%; Pred. No. 2.1e-22;
Matches 63; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

```

```

QY 27 KXSPMATVTRKAPKQIOFADDMQEFKPTKTRRSLSRSISQSTDSYSSAASYDSSD 86
DB 61 KKKYINNGNSGIAQIOFADQKQEFNKRPTKIGRSLRSISQSTDSYSSAASYDSSD 120
87 DEVSPREKQOTNSKSGSNFCVKN1 110
121 DETSPRDKQKNSKSGSDFCVKN1 144

```

```

RESULT 13
US-11-097-143-2781
; Sequence 2781, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2781
; LENGTH: 521
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-2781

```

```

Query Match      28.4%; Score 157.5; DB 6; Length 521;
Best Local Similarity 66.1%; Pred. No. 3e-07;
Matches 37; Conservative 6; Mismatches 10; Indels 3; Gaps 2;

```

```

QY 57 KTGRRSLRSISQSTDSYSSAASYDSSD--DEVSPREKQOTNSKSGSNFCVKN1 110
DB 46 KTSRYSRSLSLASSTDSFSS--ASYGSSBDCDDVPREKVKQNSKSGSDFCVKN1 100

```

```

; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; FILE REFERENCE: CL000728
; CURRENT FILING DATE: 2005-04-04
; PRIOR FILING DATE: 1999-10-05
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-19
; PRIOR FILING DATE: 1999-10-28
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-11-12
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 1999-12-28
; PRIOR FILING DATE: 2000-01-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41922
; LENGTH: 504
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-41922

```

```

Query Match      18.7%; Score 104; DB 6; Length 504;
Best Local Similarity 50.0%; Pred. No. 0.079;
Matches 24; Conservative 9; Mismatches 13; Indels 2; Gaps 2;

```

```

QY 64 SRSISQSTDSYSSAASYDSSDDE-VSPREKQOTNSKSGSNFCVKN1 110
DB 27 ARRFSDVSTCSFSTC-FTGSSDEEDVSPKDNHQRNSAGTDFCVKSI 73

```

```

RESULT 15
US-10-696-909A-46
; Sequence 46, Application US/10696909A
; Publication No. US20050118604A1
; GENERAL INFORMATION:
; APPLICANT: Lorens, James B.
; APPLICANT: Atchison, Robert E.
; APPLICANT: Fliera, Anabella
; APPLICANT: Holland, Sacha
; APPLICANT: Rigel Pharmaceuticals, Inc.
; TITLE OF INVENTION: Modulators of Angiogenesis and Tumorigenesis
; FILE REFERENCE: 021044-005820US
; CURRENT FILING DATE: 2003-10-29
; PRIOR FILING DATE: 2003-10-29
; PRIOR FILING DATE: 2003-10-17
; PRIOR FILING DATE: 2003-10-17
; PRIOR FILING DATE: 2002-10-29
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 2296
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: splicing coactivator subunit SRm300
US-10-696-909A-46

```

```

Query Match      15.7%; Score 87; DB 5; Length 2296;
Best Local Similarity 29.7%; Pred. No. 29;
Matches 27; Conservative 15; Mismatches 35; Indels 14; Gaps 2;

```

```

QY 24 DAKXSPMATV-----TKAPKQIOFADDMQEFKPTKTRRSLSRSISQSTDS 74

```

Thu Sep 7 09:46:30 2006

us-10-683-610-1_copy_1_110.rapbm

Page 6

D_b 2144 DSESSFLCUNSGIEVPSPTPAPEAVREGRPE-----ETPAKRRKRRSSSSSSSSSS 2198

Q_y 75 YSSAASYDSSDDEVSPREKQQTNSKSSNF 105
|||::|||
2199 SSSSSSSSSSSSSSSSSSSSSSSSSSSSSSF 2229

Search completed: September 6, 2006, 19:57:41
Job time : 37.587 secs


```

; SEQ ID NO 96044
; LENGTH: 602
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(602)
; OTHER INFORMATION: Ceres Seq. ID no. 12731601
US-11-056-355B-96044

Query Match          14.6%; Score 81; DB 7; Length 602;
Best Local Similarity 26.7%; Pred. No. 14;
Matches 27; Conservative 17; Mismatches 43; Indels 14; Gaps 2;

QY 14 EELKQAKEIEDAEKYSFMATVTAKPKQIQFADDMOE---FTKFPKTGRSLRSISQ 69
Db 236 EESSSDDEPPTPAKKPTVVKNAKPAKADSSSESDSEEDSEDEKPTKKAQVSKTSKOE 295
QY 70 SSTDSYSSAASYTDSDEVSDEVPREK-----OQTNSK 100
Db 296 SSSDESSDESDKESKDEKVTPKKQSDVEMVDAEQKSNK 336

RESULT 3
US-11-056-355B-96043
; Sequence 96043, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 96043
; LENGTH: 619
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(619)
; OTHER INFORMATION: Ceres Seq. ID no. 12731600
US-11-056-355B-96043

Query Match          14.6%; Score 81; DB 7; Length 619;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 27; Conservative 17; Mismatches 43; Indels 14; Gaps 2;

QY 14 EELKQAKEIEDAEKYSFMATVTAKPKQIQFADDMOE---FTKFPKTGRSLRSISQ 69
Db 253 EESSSDDEPPTPAKKPTVVKNAKPAKADSSSESDSEEDSEDEKPTKKAQVSKTSKOE 312
QY 70 SSTDSYSSAASYTDSDEVSDEVPREK-----OQTNSK 100
Db 313 SSSDESSDESDKESKDEKVTPKKQSDVEMVDAEQKSNK 353

RESULT 4
US-11-056-355B-96042
; Sequence 96042, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
```

```

; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 96042
; LENGTH: 636
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(636)
; OTHER INFORMATION: Ceres Seq. ID no. 12731599
US-11-056-355B-96042

Query Match          14.6%; Score 81; DB 7; Length 636;
Best Local Similarity 26.7%; Pred. No. 15;
Matches 27; Conservative 17; Mismatches 43; Indels 14; Gaps 2;

QY 14 EELKQAKEIEDAEKYSFMATVTAKPKQIQFADDMOE---FTKFPKTGRSLRSISQ 69
Db 270 EESSSDDEPPTPAKKPTVVKNAKPAKADSSSESDSEEDSEDEKPTKKAQVSKTSKOE 329
QY 70 SSTDSYSSAASYTDSDEVSDEVPREK-----OQTNSK 100
Db 330 SSSDESSDESDKESKDEKVTPKKQSDVEMVDAEQKSNK 370

RESULT 5
US-11-056-355B-72423
; Sequence 72423, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 72423
; LENGTH: 472
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(472)
; OTHER INFORMATION: Ceres Seq. ID no. 4932986
US-11-056-355B-72423

Query Match          14.0%; Score 77.5; DB 7; Length 472;
Best Local Similarity 26.0%; Pred. No. 22;
Matches 25; Conservative 21; Mismatches 47; Indels 3; Gaps 2;

QY 6 AMPLPGVEELKQAKEIEDAEKYSFMATVTAKPKQIQFADDMOEFTKFPKTGRSLRSISQ 64
Db 239 ASPLPRGSN--KCLRVPVLSSESDIFPSFRKTPBGRKLTKELOTKSTENALKEV 296
QY 65 RSISQSTDSYSSAASYTDSDEVSDEVPREKQQTNSK 100
Db 297 SSPBEGSSGSEKQARNGTSEPVGECTKKKKQVRVYK 332

RESULT 6
US-11-056-355B-72422
; Sequence 72422, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
```

```
FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 72422
; LENGTH: 491
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(491)
; OTHER INFORMATION: Ceres Seq. ID no. 4932985
US-11-056-355B-72422

Query Match          14.0%; Score 77.5; DB 7; Length 491;
Best Local Similarity 26.0%; Pred. No. 23;
Matches 25; Conservative 21; Mismatches 47; Indels 3; Gaps 2;

QY 6 AMPLGCVGSELKQAEIEDAEKYSFMATVTKAPKQIOFADDMQEFPTKPTGRRSLRS 64
Db 258 ASPLPRGSN-KKLRTPVLSSEDFPSSPHKTPGGRKLTKELOKFTYESTENALKEIV 315
QY 65 RSISQSTDSYSSAASYTDSDEVSPPREKQOTNSK 100
Db 316 SSPEGSSGSEKQAAKGTSPEVGECTKKKKQVRVRYK 351

RESULT 7
US-11-056-355B-72421
; Sequence 72421, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 72421
; LENGTH: 651
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(651)
; OTHER INFORMATION: Ceres Seq. ID no. 4932984
US-11-056-355B-72421

Query Match          14.0%; Score 77.5; DB 7; Length 651;
Best Local Similarity 26.0%; Pred. No. 32;
Matches 25; Conservative 21; Mismatches 47; Indels 3; Gaps 2;

QY 6 AMPLGCVGSELKQAEIEDAEKYSFMATVTKAPKQIOFADDMQEFPTKPTGRRSLRS 64
Db 418 ASPLPRGSN-KKLRTPVLSSEDFPSSPHKTPGGRKLTKELOKFTYESTENALKEIV 475
QY 65 RSISQSTDSYSSAASYTDSDEVSPPREKQOTNSK 100
Db 476 SSPEGSSGSEKQAAKGTSPEVGECTKKKKQVRVRYK 511

RESULT 8
US-11-056-355B-24462
; Sequence 24462, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
```

```
APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 24462
; LENGTH: 556
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(556)
; OTHER INFORMATION: Ceres Seq. ID no. 12336461
US-11-056-355B-24462

Query Match          13.9%; Score 77; DB 7; Length 556;
Best Local Similarity 27.4%; Pred. No. 29;
Matches 32; Conservative 14; Mismatches 35; Indels 36; Gaps 5;

QY 17 KOAKEIEDA---EKYSFMATVTKAPKQIOFADDM-----QEFPTKPTGRRSLRS 66
Db 38 KOKQDIVAAVQKEK-----AVKKVPKK-VESSDSDSESEEEKAKKVPKAKKAASSDSES 91
QY 67 ISQSTDSY-----SSAASYTDSDEVSPPREKQOTNSKGS 103
Db 92 SDDSSDDEPAPKAVATNGTVAKKSDSDSSDSDDEEVAVTKKPAALAKNGS 148

RESULT 9
US-11-056-355B-35397
; Sequence 35397, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 35397
; LENGTH: 556
; TYPE: prt
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(556)
; OTHER INFORMATION: Ceres Seq. ID no. 12336461
US-11-056-355B-35397

Query Match          13.9%; Score 77; DB 7; Length 556;
Best Local Similarity 27.4%; Pred. No. 29;
Matches 32; Conservative 14; Mismatches 35; Indels 36; Gaps 5;

QY 17 KOAKEIEDA---EKYSFMATVTKAPKQIOFADDM-----QEFPTKPTGRRSLRS 66
Db 38 KOKQDIVAAVQKEK-----AVKKVPKK-VESSDSDSESEEEKAKKVPKAKKAASSDSES 91
QY 67 ISQSTDSY-----SSAASYTDSDEVSPPREKQOTNSKGS 103
Db 92 SDDSSDDEPAPKAVATNGTVAKKSDSDSSDSDDEEVAVTKKPAALAKNGS 148

RESULT 10
US-10-449-902-34600
; Sequence 34600, Application US/10449902
```

```
/ Publication No. US20060123505A1
/ GENERAL INFORMATION:
/ APPLICANT: National Institute of Agrobiological Sciences.
/ APPLICANT: Bio-oriented Technology Research Advancement Institution.
/ APPLICANT: The Institute for Physical and Chemical Research.
/ APPLICANT: Foundation for Advancement of International Science.
/ TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
/ FILE REFERENCE: MOA-A0205Y1-US
/ CURRENT APPLICATION NUMBER: US/10/449,902
/ PRIOR FILING DATE: 2003-05-29
/ PRIOR APPLICATION NUMBER: JP 2002-203269
/ PRIOR FILING DATE: 2002-05-30
/ PRIOR APPLICATION NUMBER: JP 2002-383870
/ PRIOR FILING DATE: 2002-12-11
/ NUMBER OF SEQ ID NOS: 56791
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 34600
/ LENGTH: 409
/ TYPE: PRT
/ ORGANISM: Oryza sativa
US-10-449-902-34600

Query Match          13.8%; Score 76.5; DB 6; Length 409;
Best Local Similarity 21.3%; Pred. No. 23;
Matches 30; Conservative 16; Mismatches 44; Indels 51; Gaps 4;

QY 3 MPDAMPPLGVGEELKQAEIDAEKYSFMATVTAKPKQIOFADDMOEFTKPTKGRS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 VPFLQKLDGIDATASRAKIKESQK-----SNKAREVDDDEEAK-PAKRKRQ 314
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 LSRISQSSSTDY-----YSSAAYTSSDDEV----- 89
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 LVKATHEIQDEDEDTKSKRGKRPKTSKSGWKAAHSSGSDDDSDDEAVDKVVAEQ 374
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 90 -----SPREKQOTNSKSS 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 375 GKRRDPKQPAEAKSSSDKGS 395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-10-953-349-37175
/ Sequence 37175, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37175
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: Zea mays subsp. mays
US-10-953-349-37175

Query Match          13.8%; Score 76.5; DB 6; Length 427;
Best Local Similarity 27.1%; Pred. No. 24;
Matches 29; Conservative 12; Mismatches 35; Indels 31; Gaps 4;

QY 8 PLPGVGEELKQAEIDAEKYSFMATVTAKPKQIOFADDMOEFTKPTK-----TGRRS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 281 PLPGT--ELKEVWKADVPK-----DDKYQYTHFAHKINSFDTAPKK 320
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 LSRISQSSSTDY-----SASYTSSDDEVSPREKQOTNSKSS 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 321 LPSDSRLRPDRYALEMGDMKSGYEKSSMEERQRAEKRTREEKGA 367
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12
US-10-953-349-37174
```

```
/ Sequence 37174, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37174
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Zea mays subsp. mays
US-10-953-349-37174

Query Match          13.8%; Score 76.5; DB 6; Length 458;
Best Local Similarity 27.1%; Pred. No. 26;
Matches 29; Conservative 12; Mismatches 35; Indels 31; Gaps 4;

QY 8 PLPGVGEELKQAEIDAEKYSFMATVTAKPKQIOFADDMOEFTKPTK-----TGRRS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 312 PLPGT--ELKEVWKADVPK-----DDKYQYTHFAHKINSFDTAPKK 351
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 LSRISQSSSTDY-----SASYTSSDDEVSPREKQOTNSKSS 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 352 LPSDSRLRPDRYALEMGDMKSGYEKSSMEERQRAEKRTREEKGA 398
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 13
US-10-953-349-37173
/ Sequence 37173, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
/ NUMBER OF SEQ ID NOS: 40252
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 37173
/ LENGTH: 531
/ TYPE: PRT
/ ORGANISM: Zea mays subsp. mays
US-10-953-349-37173

Query Match          13.8%; Score 76.5; DB 6; Length 531;
Best Local Similarity 27.1%; Pred. No. 31;
Matches 29; Conservative 12; Mismatches 35; Indels 31; Gaps 4;

QY 8 PLPGVGEELKQAEIDAEKYSFMATVTAKPKQIOFADDMOEFTKPTK-----TGRRS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 385 PLPGT--ELKEVWKADVPK-----DDKYQYTHFAHKINSFDTAPKK 424
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 63 LSRISQSSSTDY-----SASYTSSDDEVSPREKQOTNSKSS 103
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 425 LPSDSRLRPDRYALEMGDMKSGYEKSSMEERQRAEKRTREEKGA 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 14
US-10-953-349-4830
/ Sequence 4830, Application US/10953349
/ Publication No. US20060107345A1
/ GENERAL INFORMATION:
/ APPLICANT: ALEXANDROV, Nickolai et al.
/ TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
/ FILE REFERENCE: 2750-1579PUS2
/ CURRENT APPLICATION NUMBER: US/10/953,349
/ CURRENT FILING DATE: 2004-09-30
```


GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:15:08 ; Search time 110.174 Seconds
(without alignments)
1161.987 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_280
Perfect score: 1461
Sequence: 1 MSMPAMPPLPGVGEELKQAK.....RLYQLSKAGKLCVPMANNVD 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq.8:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*
 - 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1461	100.0	530	7	ADB68448 Human DCA
2	1461	100.0	530	7	ADB68450 Murine DC
3	1461	100.0	530	7	ADB68452 Murine DC
4	1461	100.0	530	7	ADB68446 Human DCA
5	1461	100.0	530	8	ADPW4432 Mouse iro
6	1461	100.0	530	8	ABW80118 Tumour-as
7	1461	100.0	530	8	ADP23045 PRO polyP
8	1461	100.0	530	8	AAW56097 Amino aci
9	1298	88.8	500	2	AAW90061 Human SAM
10	1262	86.4	597	8	ADQ43989 Amino aci
11	1162	79.5	611	8	ABW80935 Tumour-as
12	1155.5	79.1	455	4	ABG12029 Novel hum
13	1140	78.0	564	5	ABG32371 Novel hum
14	1135	77.7	508	8	ADL10638 Human the
15	1135	77.7	509	8	ADL90193 Human enz
16	847	58.0	521	4	ABBS8663 Drosophil
17	772	52.8	539	4	ABR71710 Drosophil
18	746	51.1	239	3	AA556801 Human pro
19	669	45.8	317	8	ADRI0475 Human pro
20	563	38.0	502	7	ABO74755 Pseudomon
21	555	38.0	463	6	ADA33133 Acinetoba
22	549	37.6	469	8	AD524848 Bacterial
23	528.5	36.2	441	9	AB339552 L. pneumo

24	528.5	36.2	447	9	AB36129 L. pneumo
25	527	36.1	426	8	AD521102 Bacterial
26	526	36.0	447	8	ADN21030 Bacterial
27	520	35.6	433	8	ADN19777 Bacterial
28	520	35.6	433	8	ADN19772 Bacterial
29	516.5	35.4	432	4	ABR70895 Drosophil
30	511	35.0	449	8	ADN19087 Bacterial
31	511	35.0	449	9	ABD13089 S. cerevi
32	511	35.0	449	9	ABD13088 S. cerevi
33	507.5	34.7	468	9	AEA20951 Novel hum
34	505	34.6	433	5	AAE25380 Human NZM
35	504.5	34.5	457	3	AAE43614 Human can
36	504	34.5	432	7	ADP4376 Human pla
37	504	34.5	432	7	ADP76060 Wild type
38	504	34.5	432	9	ABD46678 Human S-a
39	502.5	34.4	437	8	ADN22444 Bacterial
40	500.5	34.3	432	9	ADY64952 S. mansoni
41	499	34.2	432	8	ABW82227 Tumour-as
42	499	34.2	432	8	AD588176 Human pro
43	499	34.2	432	8	ADP23057 PRO polyP
44	499	34.2	432	9	ADX07800 Cyclin-de
45	499	34.2	432	9	ADX56955 Human S-a

ALIGNMENTS

RESULT 1		ADB68448	standard; protein; 530 AA.
XX	ID	ADB68448	
XX	AC	ADB68448;	
XX	DT	04-DEC-2003	(first entry)
XX	XX		
DE	Human DCA	protein - SEQ ID 4.	
XX	XX		
KW	dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;		
KW	DC; AHCV; DCAU; anti-allergic; immunosuppressive; allergy; asthma;		
KW	allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;		
KW	rheumatoid arthritis; transplant rejection; vaccine; gene therapy; human.		
OS	Homo sapiens.		
XX	XX		
XX	Key	Location/Qualifiers	
FT	Domain	1..106	
FT	Domain	/note = Hydrophilic domain	
FT	Domain	107..530	
FT	Domain	/note = adenosine-homocysteine hydrolase (AHCV)-like	
FT	Domain	domain	
FT	Binding-site	318..323	
FT	Binding-site	/note= "NAD+ binding motif (GXGXXG)"	
FT	MO2003055997-A1.		
XX	10-JUL-2003.		
XX	24-DEC-2002; 2002WO-AU001761.		
XX	24-DEC-2001; 2001AU-00009741.		
XX	(ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.		
XX	Kato M, Angel NZ, Cooper BJ, Hart DNJ;		
XX	WPI; 2003-559275/52.		
XX	N-PSDB; ADB68445; ADB68447.		
DR	New dendritic cell expressed S-adenosyl homocysteine hydrolase-like		
XX	molecule (DCAU) gene, useful for preparing a composition for treating or		
PT	preventing a condition e.g., allergy, autoimmune disease or transplant		
PT	rejection.		

PS Disclosure; Fig 1B; 189pp; English.
XX
CC The invention relates to a novel isolated polynucleotide comprising a
CC dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-
CC like molecule (DCAL) gene. The polynucleotide of the invention
CC demonstrates anti-allergic and immunosuppressive activities and may be
CC useful for treating a condition including an allergy such as asthma,
CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
CC therapy procedures. The genetically modified animal or the identified
CC modulatory agent of the invention may be used in the study of immunity,
CC DC function, brain physiology or neuronal cell function. The current
CC sequence is that of the human DCAL protein (Seq ID 4) of the invention
CC which is encoded by the human DCAL cDNA.

XX
SQ Sequence 530 AA;

Query Match 100.0%; Score 1461; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMAVTATKAPKKQIQFADDMQEFTEPPTKGR 60
DB 1 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMAVTATKAPKKQIQFADDMQEFTEPPTKGR 60
QY 61 RSLRSISISOSTSDSYSSAASYTDSDEVS PREKOQTNKSSNFCVKNIKQAEFRRRI 120
DB 61 RSLRSISISOSTSDSYSSAASYTDSDEVS PREKOQTNKSSNFCVKNIKQAEFRRRI 120
QY 121 EIAEODMSALISLRKAOGEKPLAGAKIVGCTHTTAQTAVLITLTCALGAQCRMSACN1Y 180
DB 121 EIAEODMSALISLRKAOGEKPLAGAKIVGCTHTTAQTAVLITLTCALGAQCRMSACN1Y 180
QY 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDOGQANNILDDGGDLTHWVYK 240
DB 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDOGQANNILDDGGDLTHWVYK 240
QY 241 YPNVFKKIRGIYESVTGVHRLYQLSKAGKLCVPMANVND 280
DB 241 YPNVFKKIRGIYESVTGVHRLYQLSKAGKLCVPMANVND 280

RESULT 2

ADB68450 standard; protein; 530 AA.

XX ADB68450;

XX 04-DEC-2003 (first entry)

XX Murine DCAL protein - SEQ ID 6.

XX dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
KW DC; AHCY; DCAL; anti-allergic; immunosuppressive; allergy; asthma;
KW allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
KW rheumatoid arthritis; transplant rejection; vaccine; gene therapy;
KW murine; mouse.

XX Mus sp.

XX Key Location/Qualifiers

XX Binding-site 318..323 /note="NAD+ binding motif (EXGXGX)"

XX MO2003055997-A1.

XX 10-JUL-2003.

XX 24-DEC-2002; 2002MO-AU001761.

XX 24-DEC-2001; 2001AU-00009741.

PA (ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.

XX Kato M, Angel NZ, Cooper BJ, Hart DNU;

XX WPI; 2003-559275/52.

XX N-PSDB; ADB68449.

XX New dendritic cell expressed S-adenosyl homocysteine hydrolase-like
PT molecule (DCAL) gene, useful for preparing a composition for treating or
PT preventing a condition e.g., allergy, autoimmune disease or transplant
PT rejection.

XX Disclosure; Page 170-172; 189pp; English.

PS The invention relates to a novel isolated polynucleotide comprising a
CC dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-
CC like molecule (DCAL) gene. The polynucleotide of the invention
CC demonstrates anti-allergic and immunosuppressive activities and may be
CC useful for treating a condition including an allergy such as asthma,
CC allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as
CC diabetes mellitus or rheumatoid arthritis or transplant rejection.
CC Furthermore, the polynucleotide may be useful as a vaccine or during gene
CC therapy procedures. The genetically modified animal or the identified
CC modulatory agent of the invention may be used in the study of immunity,
CC DC function, brain physiology or neuronal cell function. The current
CC sequence is that of the murine DCAL protein (Seq ID 6) of the invention
CC which is encoded by genomic DNA.

XX Sequence 530 AA;

Query Match 100.0%; Score 1461; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMAVTATKAPKKQIQFADDMQEFTEPPTKGR 60
DB 1 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMAVTATKAPKKQIQFADDMQEFTEPPTKGR 60
QY 61 RSLRSISISOSTSDSYSSAASYTDSDEVS PREKOQTNKSSNFCVKNIKQAEFRRRI 120
DB 61 RSLRSISISOSTSDSYSSAASYTDSDEVS PREKOQTNKSSNFCVKNIKQAEFRRRI 120
QY 121 EIAEODMSALISLRKAOGEKPLAGAKIVGCTHTTAQTAVLITLTCALGAQCRMSACN1Y 180
DB 121 EIAEODMSALISLRKAOGEKPLAGAKIVGCTHTTAQTAVLITLTCALGAQCRMSACN1Y 180
QY 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDOGQANNILDDGGDLTHWVYK 240
DB 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDOGQANNILDDGGDLTHWVYK 240
QY 241 YPNVFKKIRGIYESVTGVHRLYQLSKAGKLCVPMANVND 280
DB 241 YPNVFKKIRGIYESVTGVHRLYQLSKAGKLCVPMANVND 280

RESULT 3

ADB68452 standard; protein; 530 AA.

XX ADB68452;

XX 04-DEC-2003 (first entry)

XX Murine DCAL protein - SEQ ID 8.

XX dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule;
KW DC; AHCY; DCAL; anti-allergic; immunosuppressive; allergy; asthma;
KW allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus;
KW rheumatoid arthritis; transplant rejection; vaccine; gene therapy;
KW murine; mouse.

XX Mus sp.

Key Location/Qualifiers
Binding-site 318..323
/note="NAD+ binding motif (GXGXXG)"
MO2003055997-A1.
10-JUL-2003.
24-DEC-2002; 2002MO-AU001761.
24-DEC-2001; 2001AU-00009741.
(ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Kato M, Angel NZ, Cooper BJ, Hart DNU;
WPI; 2003-559275/52.
N-PSDB; ADB684451.
New dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule (DCAL) gene, useful for preparing a composition for treating or preventing a condition e.g., allergy, autoimmune disease or transplant rejection.
Disclosure; Page 175-177; 189pp; English.
The invention relates to a novel isolated polynucleotide comprising a dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-like molecule (DCAL) gene. The polynucleotide of the invention demonstrates antiallergic and immunosuppressive activities and may be useful for treating a condition including an allergy such as asthma, allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as diabetes mellitus or rheumatoid arthritis or transplant rejection. Furthermore, the polynucleotide may be useful as a vaccine or during gene therapy procedures. The genetically modified animal or the identified modulatory agent of the invention may be used in the study of immunity, DC function, brain physiology or neuronal cell function. The current sequence is that of the murine DCAL protein (SEQ ID 8) of the invention which is encoded by cDNA.
Sequence 530 AA;
Query Match 100.0%; Score 1461; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MSMPDAMP.LPGVGEELKQAKIEDEAEKYSFMAVTYTKAPKKQIQPADMQEFTKPTKTGR 60
1 MSMPDAMP.LPGVGEELKQAKIEDEAEKYSFMAVTYTKAPKKQIQPADMQEFTKPTKTGR 60
61 RSLRSISQSSSTDYSSAASYTSSDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
61 RSLRSISQSSSTDYSSAASYTSSDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCAAGACRMSACNIY 180
121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCAAGACRMSACNIY 180
181 STONEVAALALAEAGAVFAMKGESEDDFMWCIDRCVNNMDGQAMNILLDDGDLTHMYKK 240
181 STONEVAALALAEAGAVFAMKGESEDDFMWCIDRCVNNMDGQAMNILLDDGDLTHMYKK 240
241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPMANVND 280
241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPMANVND 280
RESULT 4
ADB68446 standard; protein; 530 AA.
ADB68446;
AC ADB68446;

04-DEC-2003 (first entry)
Human DCAL protein - SEQ ID 2.
dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule; DC; AHCY; DCAL; antiallergic; immunosuppressive; allergy; asthma; allergic rhinitis; systemic anaphylaxis; autoimmune; diabetes mellitus; rheumatoid arthritis; transplant rejection; vaccine; gene therapy; human; chromosome 1p21.1.
Homo sapiens.
Location/Qualifiers
Domain 1..106
/note = Hydrophilic domain
Domain 107..530
/note = adenosine-homocysteine hydrolase (AHCY)-like domain
Binding-site 318..323
/note="NAD+ binding motif (GXGXXG)"
MO2003055997-A1.
10-JUL-2003.
24-DEC-2002; 2002MO-AU001761.
24-DEC-2001; 2001AU-00009741.
(ORDE-) ORDER OF SISTERS OF MERCY IN QUEENSLAND.
Kato M, Angel NZ, Cooper BJ, Hart DNU;
WPI; 2003-559275/52.
N-PSDB; ADB684451.
New dendritic cell expressed S-adenosyl homocysteine hydrolase-like molecule (DCAL) gene, useful for preparing a composition for treating or preventing a condition e.g., allergy, autoimmune disease or transplant rejection.
Disclosure; Fig 1B; 189pp; English.
The invention relates to a novel isolated polynucleotide comprising a dendritic cell (DC)-expressed S-adenosyl homocysteine hydrolase (AHCY)-like molecule (DCAL) gene. The polynucleotide of the invention demonstrates antiallergic and immunosuppressive activities and may be useful for treating a condition including an allergy such as asthma, allergic rhinitis or systemic anaphylaxis, an autoimmune disease such as diabetes mellitus or rheumatoid arthritis or transplant rejection. Furthermore, the polynucleotide may be useful as a vaccine or during gene therapy procedures. The genetically modified animal or the identified modulatory agent of the invention may be used in the study of immunity, DC function, brain physiology or neuronal cell function. The current sequence is that of the human DCAL protein (SEQ ID 2) of the invention which is encoded by DNA localised to chromosome 1p21.1.
Sequence 530 AA;
Query Match 100.0%; Score 1461; DB 7; Length 530;
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MSMPDAMP.LPGVGEELKQAKIEDEAEKYSFMAVTYTKAPKKQIQPADMQEFTKPTKTGR 60
1 MSMPDAMP.LPGVGEELKQAKIEDEAEKYSFMAVTYTKAPKKQIQPADMQEFTKPTKTGR 60
61 RSLRSISQSSSTDYSSAASYTSSDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
61 RSLRSISQSSSTDYSSAASYTSSDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCAAGACRMSACNIY 180
121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVALIETLCAAGACRMSACNIY 180

Db 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRWSACN1Y 180
 QY 181 STONEVAALAAEAGVAVFAWKGSEDDFWWCIDRCVNMWGQANNILDDGGDLTHVYKK 240
 Db 181 STONEVAALAAEAGVAVFAWKGSEDDFWWCIDRCVNMWGQANNILDDGGDLTHVYKK 240
 QY 241 YPNVFKKIRGIIEESVTGVHRLYQLSKAGKLCVPMANVND 280
 Db 241 YPNVFKKIRGIIEESVTGVHRLYQLSKAGKLCVPMANVND 280
 RESULT 5
 ADM94432
 ID ADM94432 standard; protein; 530 AA.
 XX ADM94432;
 AC ADM94432;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Mouse inositol 1,4,5-triphosphate receptor binding protein.
 XX
 KM inositol-triphosphate receptor-binding protein; IP3 receptor;
 KM fluorescence resonance energy transfer; IP3 quantification;
 KM IP3-induced Ca²⁺ releasing activity; PIP2 function.
 XX
 OS Mus musculus.
 XX
 PI EPI408049-A2.
 XX
 PD 14-APR-2004.
 XX
 PF 13-OCT-2003; 2003EP-00256457.
 XX
 PR 11-OCT-2002; 2002UP-00299429.
 XX
 PA (RIKE) RIKEN KK.
 XX
 PI Mikoshiba K, Ando H, Mizutani A, Matsui-Ura T;
 DR WPI; 2004-349314/33.
 XX
 DR N-PSDB; ADM94433.
 XX
 PT New inositol 1,4,5-triphosphate receptor-binding protein that binds to
 PT inositol 1,4,5-triphosphate receptor, useful as inositol 1,4,5-
 PT triphosphate indicator intracellularly and in cell-free system.
 XX
 PS Claim 1; SEQ ID NO 1; 61pp; English.
 XX
 CC The invention relates to a novel inositol 1,4,5-triphosphate (IP3)
 CC receptor-binding protein (I) that binds to IP3 receptor. (I) is used as
 CC an IP3 indicator in combination with a fluorescent molecule for detecting
 CC IP3 by the fluorescence resonance energy transfer (FRET) method using a
 CC combination of two fluorescent molecules applicable to the FRET method,
 CC and a protein containing at least IP3-binding domain of IP3 receptor
 CC labelled with the other fluorescent molecule. (I) is useful as IP3
 CC indicator intracellularly and in cell-free system, for detecting and/or
 CC quantifying IP3, as modulator of IP3-induced Ca²⁺ releasing activity,
 CC modulator of PIP2 function and Na²⁺ and bicarbonate ions. This sequence
 CC represents the IP3 receptor binding protein.
 XX
 XX Sequence 530 AA;
 SQ
 Query Match 100.0%; Score 1461; DB 8; Length 530;
 Best Local Similarity 100.0%; Pred. No. 8.2e-146;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMPDMPPIPGVGEELKQAKETEDARKYSFMAVTATKAPKKQIOFADMOEFTPKTKGR 60
 Db 1 MAMPDMPPIPGVGEELKQAKETEDARKYSFMAVTATKAPKKQIOFADMOEFTPKTKGR 60
 QY 61 RLSRSRISQSSSTDSYSSAASYTDSDEVPREKQOTNSKGSNFCVKKIKQAEFGRRRI 120
 Db 61 RLSRSRISQSSSTDSYSSAASYTDSDEVPREKQOTNSKGSNFCVKKIKQAEFGRRRI 120

QY 121 EIAEQDMSALISLRRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRWSACN1Y 180
 Db 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRWSACN1Y 180
 QY 181 STONEVAALAAEAGVAVFAWKGSEDDFWWCIDRCVNMWGQANNILDDGGDLTHVYKK 240
 Db 181 STONEVAALAAEAGVAVFAWKGSEDDFWWCIDRCVNMWGQANNILDDGGDLTHVYKK 240
 QY 241 YPNVFKKIRGIIEESVTGVHRLYQLSKAGKLCVPMANVND 280
 Db 241 YPNVFKKIRGIIEESVTGVHRLYQLSKAGKLCVPMANVND 280
 RESULT 6
 ABM80118
 ID ABM80118 standard; protein; 530 AA.
 XX ABM80118;
 AC ABM80118;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO80619, SEQ.301.
 XX
 KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukaemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PI WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GENTH) GENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 DR WPI; 2004-347921/32.
 XX
 DR N-PSDB; ACN37426.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 301; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be

CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a 1AT polypeptide of the invention

Sequence 530 AA;

Query Match 100.0%; Score 1461; DB 8; Length 530;
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPPLPGVGEELKQAKIEIDAEKYSFMAVTTKAPKKOIQFADDMQEFKFTKGR 60
DB 1 MSMPDAMPPLPGVGEELKQAKIEIDAEKYSFMAVTTKAPKKOIQFADDMQEFKFTKGR 60
QY 61 RLSRSISQSSSTDYSYSSAASVTDSDEVS PREKQNTSKSSNFCVKNIKOAEGRREI 120
DB 61 RLSRSISQSSSTDYSYSSAASVTDSDEVS PREKQNTSKSSNFCVKNIKOAEGRREI 120
QY 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCALGACRWSACNII 180
DB 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCALGACRWSACNII 180
QY 181 STONEVAAAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGDLTHWVYK 240
DB 181 STONEVAAAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGDLTHWVYK 240
QY 241 YPNVFKIKIRGIVESVTGVHRLYOLSKAGKLCVPMANVND 280
DB 241 YPNVFKIKIRGIVESVTGVHRLYOLSKAGKLCVPMANVND 280

RESULT 7
ADP23045
ID ADP23045 standard; protein; 530 AA.

XX ADP23045;
XX 18-NOV-2004 (first entry)
XX PRO polypeptide SEQ ID NO:139.
XX PRO: antiinflammatory; antiaerthritic; antirheumatic; immunosuppressive;
XX osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX antiaesthetic; hepatotropic; respiratory; gene therapy; immune system.
XX Unidentified.
XX OS
XX WO2004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH) GENENTECH INC.
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX MU TD;
XX WPI, 2004-419628/39.
XX DR N-PSDB; ADP23044.
XX PT New PRO polypeptides and polynucleotides, useful for treating e.g.
XX PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX PT renal disease, or demyelinating diseases of the central or peripheral
XX PT nervous system.
XX Claim 7; SEQ ID NO 139; 2940pp; English.
XX The invention relates to a novel isolated nucleic acid and the PRO
XX polypeptide encoded by it. A protein of the invention has
XX antiinflammatory, antiaerthritic, antirheumatic, immunosuppressive,

CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
CC antiaesthetic, hepatotropic, and respiratory activity. A polynucleotide
CC of the invention may have a use in gene therapy. The PRO polypeptide, its
CC agonist, antagonist, or antibody that specifically binds to the
CC polypeptide is useful for treating an immune related disorder such as
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
CC idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
CC disease, a demyelinating disease of the central or peripheral nervous
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
CC disease, infectious or autoimmune chronic active hepatitis, primary
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
CC disease, asthma, allergic rhinitis, atopic dermatitis, food
CC hypersensitivity, urticaria, an immunologic disease of the lung,
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
CC pneumonitis, a transplantantion associated disease, graft rejection or
CC graft-versus-host disease. The present sequence represents a PRO protein
CC of the invention.

Sequence 530 AA;

Query Match 100.0%; Score 1461; DB 8; Length 530;
Best Local Similarity 100.0%; Pred. No. 8.2e-146;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPPLPGVGEELKQAKIEIDAEKYSFMAVTTKAPKKOIQFADDMQEFKFTKGR 60
DB 1 MSMPDAMPPLPGVGEELKQAKIEIDAEKYSFMAVTTKAPKKOIQFADDMQEFKFTKGR 60
QY 61 RLSRSISQSSSTDYSYSSAASVTDSDEVS PREKQNTSKSSNFCVKNIKOAEGRREI 120
DB 61 RLSRSISQSSSTDYSYSSAASVTDSDEVS PREKQNTSKSSNFCVKNIKOAEGRREI 120
QY 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCALGACRWSACNII 180
DB 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCALGACRWSACNII 180
QY 181 STONEVAAAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGDLTHWVYK 240
DB 181 STONEVAAAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGDLTHWVYK 240
QY 241 YPNVFKIKIRGIVESVTGVHRLYOLSKAGKLCVPMANVND 280
DB 241 YPNVFKIKIRGIVESVTGVHRLYOLSKAGKLCVPMANVND 280

RESULT 8

AAWS6097
ID AAWS6097 standard; protein; 614 AA.

XX AAWS6097;
XX 21-AUG-1998 (first entry)
XX Amino acid sequence of the ODD4b5.3 enzyme.
XX DD4b9.3 enzyme; S-adenosyl-L-homocysteine hydrolase-type activity;
XX AHcy-type activity; stimulation; inhibition; dendritic cell; cancer;
XX autoimmune disease; transplantation.
XX Homo sapiens.
XX PN WO9814562-A1.
XX PD 09-APR-1998.
XX PF 06-OCT-1997; 97WO-NZ000133.

XX PR 04-OCT-1996; 96NZ-00299507.
XX (HART/) HART D N J.
XX PI Hart DNT;
XX DR WPI; 1998-240074/21.
XX DR N-PSDB; AAV28617.
XX PT New isolated S-adenosyl-L-homocysteine hydrolase enzyme - is used to
XX PT develop products which can be used in the treatment of e.g. auto-immune
XX PT disease, transplantsations or cancers.
XX PS Claim 3; Fig 1; 33pp; English.
XX CC This is the amino acid sequence of the DP4b9.3 enzyme which has S-
XX CC adenosyl-L-homocysteine hydrolase (AHCY)-type activity. Its products can
XX CC be used to identify substances which have a stimulatory or inhibitory
XX CC effect on the enzyme activity. Such substances can be used to modulate
XX CC dendritic cell (DC) function and for immunomodulation. They can be used
XX CC in the treatment of e.g. autoimmune diseases, transplantsations or
XX CC cancers. The products can also be used for detection and diagnosis
XX SQ Sequence 614 AA;
XX
XX Query Match 100.0%; Score 1461; DB 2; Length 614;
XX Best Local Similarity 100.0%; Pred. No. 1e-145;
XX Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIOFADDMOEFTFPTKTGR 60
XX |
XX DB 85 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIOFADDMOEFTFPTKTGR 144
XX |
XX QY 61 RLSRSRISOSSTSYSSAASYTDSDEVS PREKQOTNSGSSNFCVKNIKQAEFGRREI 120
XX |
XX DB 145 RLSRSRISOSSTSYSSAASYTDSDEVS PREKQOTNSGSSNFCVKNIKQAEFGRREI 204
XX |
XX QY 121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHITTAQTAVLIELTLCALGAQCRWSACNII 180
XX |
XX DB 205 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHITTAQTAVLIELTLCALGAQCRWSACNII 264
XX |
XX QY 181 STONEVAALAEAGVAVFAMKGESEDDFWWCICRCVNMDSQANMILDDGGDLTHWYKK 240
XX |
XX DB 265 STONEVAALAEAGVAVFAMKGESEDDFWWCICRCVNMDSQANMILDDGGDLTHWYKK 324
XX |
XX QY 241 YPVVFKIRIGIVESVTGVHRLYQLSKAGKLCVPAANVND 280
XX |
XX DB 325 YPVVFKIRIGIVESVTGVHRLYQLSKAGKLCVPAANVND 364
XX |
XX
XX RESULT 9
XX AAM90061
XX ID AAM90061 standard; protein; 500 AA.
XX AC AAM90061;
XX DT 04-MAR-1999 (first entry)
XX DE Human SAHH protein.
XX KW S-adenosyl-5-homocysteine hydrolase; SAHH, human; drug screening;
XX KW treatment; infection; cancer; autoimmune disease; detection; diagnosis;
XX KW gene mapping; antisense; therapy; antagonist; immunoassay.
XX OS Homo sapiens.
XX XX US5854023-A.
XX XX 29-DEC-1998.
XX PD 17-JUL-1997; 97US-00896005.
XX PF
XX XX

PR 17-JUL-1997; 97US-00896005.
XX (INCY-) INCYTE PHARM INC.
XX PA Shah P, Lal P, Hillman JL, Corley NC;
XX PI WPI; 1999-094906/08.
XX DR N-PSDB; AAV73924.
XX PT Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase - for
XX PT production of recombinant enzyme, useful for diagnosis, treatment and
XX PT prevention of cancers, infections and autoimmune diseases.
XX PS Claim 1; Fig 1A-I; 40pp; English.
XX
XX CC This sequence represents a human S-adenosyl-5-homocysteine hydrolase
XX CC (SAHH). The SAHH protein can be used to generate specific antibodies and
XX CC in drug screening to identify specific binding agents. Antagonists of the
XX CC protein are used to treat or prevent a wide range of viral, bacterial,
XX CC fungal, parasitic, protozoal or helminthic infections, many cancers
XX CC (leukaemia, lymphoma or solid tumours), and many autoimmune diseases
XX CC (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes
XX CC mellitus, multiple sclerosis etc). All these conditions may be treated by
XX CC expressing antisense sequences, triplex-forming agents or ribozymes
XX CC directed against the nucleic acid. The nucleic acid and its fragments can
XX CC be used as probes or primers for detecting and quantifying gene
XX CC expression, for diagnosis or monitoring of disease, to identify genetic
XX CC variations, mutations or polymorphisms, in gene mapping and as antisense
XX CC therapeutics. Antibodies are used directly as antagonists, indirectly to
XX CC deliver active agents to SAHH-expressing cells, to diagnose and monitor
XX CC diseases in standard immunoassays, in competitive drug screens and to
XX CC isolate the protein from natural sources
XX SQ Sequence 500 AA;
XX
XX Query Match 88.8%; Score 1298; DB 2; Length 500;
XX Best Local Similarity 99.6%; Pred. No. 1.6e-128;
XX Matches 249; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 31 MATVTAKPKKQIOFADDMOEFTFPTKTGRSLRSISQSSYDSSAASYTDSDEVS 90
XX |
XX DB 1 MATVTAKPKKQIOFADDMOEFTFPTKTGRSLRSISQSSYDSSAASYTDSDEVS 60
XX |
XX QY 91 PREKQOTNSGSSNFCVKNIKQAEFGRREIEIAEDMSALISLRKQAGEKPLAGAKIVG 150
XX |
XX DB 61 PREKQOTNSGSSNFCVKNIKQAEFGRREIEIAEDMSALISLRKQAGEKPLAGAKIVG 120
XX |
XX QY 151 CTHITTAQTAVLIELTLCALGAQCRWSACNIIYSTONEVAALAEAGVAVFAMKGESEDDFW 210
XX |
XX DB 121 CTHITTAQTAVLIELTLCALGAQCRWSACNIIYSTONEVAALAEAGVAVFAMKGESEDDFW 180
XX |
XX QY 211 CIDRCVNMDSQANMILDDGGDLTHWYKKYPNVFKIRIGIVESVTGVHRLYQLSKAGK 270
XX |
XX DB 181 CIDRCVNMDSQANMILDDGGDLTHWVCKKYPNVFKIRIGIVESVTGVHRLYQLSKAGK 240
XX |
XX QY 271 LCVPAANVND 280
XX |
XX DB 241 LCVPAANVND 250
XX |
XX
XX RESULT 10
XX ADO43989
XX ID ADO43989 standard; protein; 597 AA.
XX AC ADO43989;
XX DT 15-JUL-2004 (first entry)
XX DE Amino acid sequence of human putative S-adenosylhomocysteinease.
XX KW protein complex; neurological disease; stroke; neurodegeneration;
XX KW Wallerian degeneration; Alzheimer's disease; neurological disorder;
XX KW epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;
XX KW

atherosclerosis; ID-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2; ASK3; CAMKII beta; CAMKII delta; CAMKII gamma; casein kinase II alpha; Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP; FLJ14653 NT2RP2002252; FLJ30839 FEBRA2002429; HERC2; inositol polyphosphate-5-phosphatase; inositol-1; 4; 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030; Nek3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor; Pushover; S-adenosylhomocysteine; secretory carrier-associated membrane protein 2; surfactant protein 2; ubiquitin carboxyl terminal hydrolase 1; upstream regulatory element binding protein 1; Vartul; Werner's syndrome helicase interacting protein; WHIP; X-ray repair cross complementing protein 4.

XX Homo sapiens.

XX WO2004031242-A2.

XX 15-APR-2004.

XX 11-SEP-2003; 2003WO-EP010110.

XX 12-SEP-2002; 2002EP-00020495.

XX 12-SEP-2002; 2002EP-00020496.

XX 12-SEP-2002; 2002EP-00020497.

XX (CELL-) CELLZONE AG.

XX Bouwmeester T, Drees G, Jackson D, Helftenbein G, Schirle M, Kuester B, Hopf C; WPI; 2004-316467/29.

XX New complex comprising at least one first protein, and at least one second protein, useful for treating stroke, Alzheimer's disease, neurological disorders such as epilepsy, and inflammatory conditions such as ulcerative colitis.

XX Example; Page 191-193; 287pp; English.

XX The specification describes protein complexes involved in cellular processes which have been shown to be critical for the development of various forms of neurological diseases. Three protein complexes were identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3 protein complex. The protein complex are useful for treating diseases and disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration, Alzheimer's disease, neurodegeneration such as epilepsy, and inflammatory conditions such as ulcerative colitis, Crohn's disease or atherosclerosis. Proteins identified as being part of the protein complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A, ASK1, ASK2, ASK3, CAMKII beta, CAMKII delta, CAMKII gamma, casein kinase II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP, FLJ14653 NT2RP2002252, FLJ30839 FEBRA2002429, HERC2, two hypothetical proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase, inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441, MSTP030, Nek3, Pellino 1, Pellino 3, podocalyxin-like protein 1 precursor, Pushover, a putative S-adenosylhomocysteine, secretory carrier-associated membrane protein 2, surfactant protein 2, ubiquitin carboxyl terminal hydrolase 1, upstream regulatory element binding protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP), X-ray repair cross complementing protein 4 (isofom 1). The present sequence represents putative S-adenosylhomocysteine.

XX Sequence 597 AA;

Query Match 86.4%; Score 1262; DB 8; Length 597;
Best Local Similarity 80.0%; Pred. No. 1,4e-124;
Matches 252; Conservative 8; Mismatches 19; Indels 36; Gaps 4;

1 MSMDPMLP-----GVGE---ELKQAKETDEAKYKSFNATVTKAPKK-----40
34 ISOP-ALPLPQETQAPSGEENLRMLRQGRRAESSQNLISLRILVSAGNGSRDWRWIMI 92

41 -----QIQPADMOEFTKPTKGRSRISRSISQSTDSYSSAASYTDS 85
93 QIMPEIDLEISCFQIQIPADMOEFTKPTKGRSRISRSISQSTDSYSSAASYTDS 152
86 DDEVSPREKQOTNSKGSNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAG 145
153 DDEVSPREKQOTNSKGSNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAG 212
146 AKIVGCTHITVQTAVALIETLCALGAQCWSACNISTONEVAALAEAGVAFPAKGESE 205
213 AKIVGCTHITVQTAVALIETLCALGAQCWSACNISTONEVAALAEAGVAFPAKGESE 272
206 DDFWMCIDRCVNMDSQNMMLDDGGDLTHWYKKYPNVFKIRGIVESVTVGVRLYOL 265
273 DDFWMCIDRCVNMDSQNMMLDDGGDLTHWYKKYPNVFKIRGIVESVTVGVRLYOL 332
266 SKAGKLCVPAWNVND 280
333 SKAGKLCVPAWNVND 347

RESULT 11
ABM80935
ID ABM80935 standard; protein; 611 AA.
XX ABM80935;
DT 18-NOV-2004 (first entry)
DE Tumour-associated antigenic target (TAT) polypeptide PRO81608, SEQ.2410.
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX tumour; diagnosis; cell proliferative disorder; breast cancer;
XX colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX central nervous system cancer; bladder cancer; pancreatic cancer;
XX cervical cancer; melanoma; leukaemia; hybridisation probe;
XX chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic.

XX Homo sapiens.

XX WO2004030615-A2.
XX 15-APR-2004.
XX 29-SEP-2003; 2003WO-US028547.
XX 02-OCT-2002; 2002US-0414971P.
XX (GETH) GENENTECH INC.
XX Wu TD, Zhang Z, Zhou Y;
XX WPI; 2004-347921/32.
XX N-PSDB; ACN38718.

XX New tumour-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
XX proliferative disorder, e.g. breast, lung, colorectal, ovarian or
XX prostate cancer or tumor.

XX Claim 12; SEQ ID NO 2410; 7273pp; English.

XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acid and polypeptide
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or

CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention

XX Sequence 611 AA;

Query Match 79.5%; Score 1162; DB 8; Length 611;
Best Local Similarity 75.7%; Pred. No. 6,4e-114;
Matches 228; Conservative 22; Mismatches 23; Indels 28; Gaps 3;

QY 8 PLPGVGE-----ELKQAKIEDDAEKY-----SFMATYTKAP---K 39
DB 61 PVPGPGSPAAALSPAAKVPQASAMKRSDPHNOHRHDGEGALVSPDGTVEARPTVK 120
QY 40 KQIQFADMDQEFPTKPTGTGRSLRSISQSSSTDYSASAAYTSSDDEVSPREKQNTS 99
DB 121 KQIQFADQKQEFNKRPTKIGRSLRSISQSSSTDYSASAAYTSSDDEVSPREKQNTS 180
QY 100 KGSNFCVKNIKQAEFGRRREIETABODMSALSLKRAQGEKPLAGAKIYGCCHITQTA 159
DB 181 KGSNDPCVKNIKQAEFGRRREIETABODMSALSLKRAQGEKPLAGAKIYGCCHITQTA 240
QY 160 VLIETLCALGAQCRWSACNIYSTONEVAALAEAGYAVFAMKGESEDDFWMCIDRCVNM 219
DB 241 LMETLGAALGAQCRMAACNISTLNEVAALAEAGYAVFAMKGESEDDFWMCIDRCVNE 300
QY 220 GQOANMILDDGDLTHWVYKYPNVFKIRGIVEESYTGVRHLVQLSKAKLQVPAANNV 279
DB 301 GQOANMILDDGDLTHWVYKYPNVFKIRGIVEESYTGVRHLVQLSKAKLQVPAANNV 360
QY 280 D 280
DB 361 D 361

RESULT 12

ABG12029
ID ABG12029 standard; protein; 455 AA.

AC ABG12029;

XX 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #12020.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KM Food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

PF 30-MAR-2001; 2001MO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Dmanac RT, Liu C, Tang YT;

XX MPI; 2001-639362/73.

XX N-PSDB; AAS76216.

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

PS Claim 20; SEQ ID NO 42388; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed.
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 455 AA;

Query Match 79.1%; Score 1155.5; DB 4; Length 455;
Best Local Similarity 75.3%; Pred. No. 2e-113;
Matches 226; Conservative 24; Mismatches 23; Indels 27; Gaps 3;

QY 8 PLPGVGE-----ELKQAKIEDDAEKY-----SFMATYTKAP---K 40
DB 61 PVPGPGSPAAALSPAAKVPQASAMKRSDPHNOHRHDGEGALVSPDGTVEARPTVK 120
QY 41 QIQFADMDQEFPTKPTGTGRSLRSISQSSSTDYSASAAYTSSDDEVSPREKQNTSK 100
DB 121 KQIQFADQKQEFNKRPTKIGRSLRSISQSSSTDYSASAAYTSSDDEVSPREKQNTSK 180
QY 101 GGSNFCVKNIKQAEFGRRREIETABODMSALSLKRAQGEKPLAGAKIYGCCHITQTA 160
DB 181 GGSNFCVKNIKQAEFGRRREIETABODMSALSLKRAQGEKPLAGAKIYGCCHITQTA 240
QY 161 LLIETLCALGAQCRWSACNIYSTONEVAALAEAGYAVFAMKGESEDDFWMCIDRCVNM 220
DB 241 LMETLGAALGAQCRMAACNISTLNEVAALAEAGYAVFAMKGESEDDFWMCIDRCVNE 300
QY 221 GQOANMILDDGDLTHWVYKYPNVFKIRGIVEESYTGVRHLVQLSKAKLQVPAANNV 280
DB 301 GQOANMILDDGDLTHWVYKYPNVFKIRGIVEESYTGVRHLVQLSKAKLQVPAANNV 360

RESULT 13

ABG32371
ID ABG32371 standard; protein; 564 AA.

AC ABG32371;

XX 15-NOV-2002 (first entry)

DE Novel human enzyme, NZMS-1, Incyte 7484737CD1.

XX Human; NZMS-1; immune system disorder; AIDS; contact dermatitis;

KM acquired immune deficiency syndrome; Chediak-Higashi syndrome;

KM common variable immunodeficiency; developmental disorder; cataract;

KM Cushing's syndrome; hypothyroidism; eye disorder; glaucoma; asthma;

KM metabolic disorder; cystic fibrosis; sickle-cell anaemia; epilepsy;

KM smooth muscle disorder; lactic acidosis; neurological disorder;

KM Parkinson's disease; cardiac disorder; congestive heart failure;

myocardial infection; pulmonary disorder; emphysema; bronchitis;
KW parasitic infection; amoebiasis; filariasis; cancer; leukaemia;
KW cell proliferative disorder; Incyte 7484737CD1; enzyme.
OS Homo sapiens.
XX MO200264795-A2.
XX
XX 22-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-US003814.
XX PF
XX 09-FEB-2001; 2001US-0268113P.
XX PR 15-FEB-2001; 2001US-0269215P.
XX PR 27-FEB-2001; 2001US-0272271P.
XX PR 07-MAR-2001; 2001US-0274091P.
XX PR 09-MAR-2001; 2001US-0274423P.
XX PR 23-MAR-2001; 2001US-0278479P.
XX PR 23-MAR-2001; 2001US-0278480P.
XX
XX (INCYTE GENOMICS INC.
XX
XX Sanjanwala MM, Lu Y, Lee EA, Hafalia AJA, Warren BA, Baughn MR;
PI Tang TY, Yue H, Yao MG, Lee S, Thornton M, Walla NK, Xu Y;
PI Tran UK, Lal PG, Lu DAM, Swarnaker A, Jones KA, Ring HZ;
XX
XX WPI; 2002-643488/69.
XX N-PSDB; ABK91312.
XX
XX New isolated human enzymes (NZMS), useful for diagnosing, treating and
PT preventing immune system, developmental, eye, metabolic, smooth muscle,
PT neurological, pulmonary and cardiac disorders, cancer, or parasitic
PT infections.

Claim 1; Page 147-149; 170pp; English.

The invention relates to a new isolated human enzyme (NZMS) (I) and the
CC encoding nucleic acid (II). The polypeptides and polynucleotides are
CC useful in assessing the effects of exogenous compounds on the expression
CC of nucleic acid and amino acid sequences of NZMS. The NZMS or its
CC fragments are useful in screening compounds for effectiveness as agonist
CC or antagonist of the polypeptides, or in altering the expression of the
CC target polynucleotide and compounds that specifically bind to or modulate
CC the activity of the polypeptide. The antibody is useful in diagnosing a
CC condition or disease associated with the decreased expression or
CC overexpression of NZMS and in detecting (I). (I) is useful in the
CC production of antibodies. The microarray is useful in monitoring or
CC measuring gene expression profiles. The polypeptides and polynucleotides
CC are useful in diagnosing, treating and preventing diseases or conditions
CC associated with the decreased expression or overexpression of NZMS, such
CC as immune system disorders (e.g. acquired immune deficiency syndrome
CC (AIDS), contact dermatitis), immune deficiencies (e.g. common variable
CC immunodeficiency, Chediak-Higashi syndrome), developmental disorders
CC (e.g. Cushing's syndrome, hypothyroidism), eye disorders (e.g. glaucoma,
CC cataract), metabolic disorders (e.g. cystic fibrosis, sickle-cell
CC anaemia), smooth muscle disorders (e.g. asthma, lactic acidosis),
CC neurological disorders (e.g. Parkinson's disease, epilepsy), cardiac
CC disorders (e.g. congestive heart failure, myocardial infarction),
CC pulmonary disorders (emphysema, bronchitis), parasitic infections
CC (leishmaniasis, filariasis), and cell proliferative disorders (e.g. cancer,
CC leukaemia). The microarray is useful in monitoring or measuring protein-
CC protein interactions, drug-target interactions, and gene expression
CC profiles. The present sequence represents the amino acid sequence of one
CC of 11 novel human enzymes (NZMS1-11) of the invention

Sequence 564 AA;

Query Match 78.0%; Score 1140; DB 5; Length 564;
Best Local Similarity 85.0%; Pred. No. 1.2e-111;
Matches 216; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

27 KSFMAVTAKPKQIQFADDMQEFKPKPTKGRSLSSISQSDSYSSAASYDSSD 86
| :: ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 61 KKKYIVNGNSGIKAQIQFADQKQEFNKPTKIGRSLSSISQSDSYSSAASYDSSD 120
QY 87 DEVSPREKQQTNSKSGSNFCVNNIKQAEFGRRREIEIAEDMSALSLRKRAQCEKPLAGA 146
Db 121 DETSPRDKQKSKSGSDFCVNNIKQAEFGRRREIEIEIAEQEMPALMLRRRAQCEKPLAGA 180
QY 147 KIVGCTHITAGTAVVLEITLCALGAOCRMWACNISTONVAAALAAAGVAFPMKGESED 206
Db 181 KIVGCTHITAGTAVVLEITLCALGAOCRMWACNISTONVAAALAAAGVAFPMKGESED 240
QY 207 DFMWCIDRCVNMDDGMQANMILDDGDLTHWYKKYPNVFKIRGIVEBSVTGVRPLYOLS 266
Db 241 DFMWCIDRCVNVBGMQPNMILDDGGDLTHWYKKYPNVFKIRGIVEBSVTGVRPLYOLS 300
QY 267 KAGKLCVPMANVND 280
Db 301 KAGKLCVPMANVND 314

RESULT 14

ADSI0638
ID ADSI0638 standard; protein; 508 AA.
XX
XX ADSI0638;
AC
XX
XX 16-DEC-2004 (first entry)
DT
XX
XX Human therapeutic protein - SEQ ID 875.
DE
XX
XX antiinflammatory; neuroprotective; antianaemic; cyostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
XX
XX Homo sapiens.
OS
XX
XX WO2004080148-A2.
XX
XX 23-SEP-2004.
XX
XX 30-SEP-2003; 2003WO-US030720.
XX
XX 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
PA
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
PI
XX
XX WPI; 2004-668857/65.
XX N-PSDB; ADS09954.
XX

New polynucleotide, useful in preparing a composition for diagnosing or
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
PT aplastic anemia or cancer for promoting wound healing.

Claim 20; SEQ ID NO 875; 718pp; English.

The invention relates to a novel isolated polynucleotide and the encoded
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,
CC neuroprotective, antianaemic, cyostatic and vulnerary activities and may
CC be useful in preparing a composition for diagnosing or treating
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic protein
CC of the invention. The current sequence is not shown explicitly within the
CC specification but can be accessed from the WIPO web-site.

Sequence 508 AA;

Query Match 77.7%; Score 1135; DB 8; Length 508;
Best Local Similarity 88.1%; Pred. No. 3.6e-111;
Matches 214; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 38 PKQIQFADDMQEFTEPKTKGRSLRSISQSSTDSYSSAASYTSSDDEVSPPREKQOT 97
DB 16 PEMWIOFADQKOFENKRPFKIGRRSLRSISQSSTDSYSSAASYTSSDDETSPPRDKQOK 75
QY 98 NSGSSNFCVKNIKQAEFRREIEIAEODMSALISLRKXQGEKPLAGAKIVGCTHITTAQ 157
DB 76 NSKSSDFCVKNIKQAEFRREIEIAEODMPALMRKRAQGEKPLAGAKIVGCTHITTAQ 135
QY 158 TAVLIETLCALGAOCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWMCIDRCVN 217
DB 136 TAVLMETLGLAGOCRMAACNIYSTLNEVAALAESEGFVFAWKGESEDDFWMCIDRCVN 135
QY 218 MDGMQANMILDDGGDLTHWVYKXYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANM 277
DB 196 VEGMQPMTILDGDDLTHWVYKXYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANM 255
QY 278 VND 280
DB 256 VND 258

RESULT 15
ADL90193 standard; protein; 509 AA.
ID ADL90193
AC ADL90193;
XX
XX
XX 17-JUN-2004 (first entry)
XX
XX Human enzyme, ENZM-3, SEQ ID 3.
XX
XX Cytostatic; Antiarteriosclerotic; Anticonvulsant; Nootropic;
XX Neuroprotective; Cerebroprotective; Anti-HIV; Antiallergic;
XX Antiinflammatory; Thyromimetic; Gene therapy; human; enzyme;
XX Cell proliferative disorder; cancer; atherosclerosis;
XX neurological disorder; epilepsy; Huntington's disease; stroke;
XX immune disorder; inflammatory disorder; AIDS; allergies;
XX developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX ENZM-3.
XX
XX Homo sapiens.
XX
XX WO2004027022-A2.
XX
XX
XX 01-APR-2004.
XX
XX 05-SEP-2003; 2003WO-US028177.
XX
XX 05-SEP-2002; 2002US-0408747P.
XX 28-OCT-2002; 2002US-0422062P.
XX 29-OCT-2002; 2002US-0422276P.
XX 13-DEC-2002; 2002US-0433388P.
XX 13-JAN-2003; 2003US-0439977P.
XX 15-JAN-2003; 2003US-0440860P.
XX 31-JAN-2003; 2003US-0444282P.
XX 04-FEB-2003; 2003US-0445371P.
XX
XX (INCY-) INCYTE CORP.
XX
XX Sanjanwala MM, Lee S, Lee SY, Tran UK, Lu Y, Baughn MR;
PI Chawla NK, Lal PG, Ring HZ, Yang YG, Hafalia AJA, Yao MG;
PI Swarnakar A, Ison CH, Chang H, Ramkumar J, Khare R, Bhatia UG;
PI Burtrill JD, Blake JT, Ho A, Zheng W, Jiang X, Jackson AA;
PI Marquis JP, Jin P, Wilson AD, Favero KD, Wang JT, Becha SD;
PI Naidu S, Yue H, Griffin JA, Kable AE, Emerling BM, Lee EA, Tang YT,
PI Li JX, Forsythe JI;
XX
XX WPI, 2004-285399/27.
XX
XX N-PSDB; ADL90239.
XX
XX New human enzymes (ENZM), useful for diagnosing, treating and preventing
PT diseases or conditions associated with the aberrant ENZM expression e.g.

PT cancer, AIDS, epilepsy, or infections.
XX
XX
XX Claim 1; SEQ ID NO 3; 344pp; English.
XX
XX
CC The present invention relates to human enzymes (ENZM-1 - ENZM-46, CC
CC ADL90193-ADL90236) and their coding sequences (ADL90237-ADL90282). The CC
CC sequences are useful in diagnosing, treating and preventing diseases or CC
CC conditions associated with the decreased expression or overexpression of CC
CC the enzymes, such as cell proliferative (e.g. cancer, atherosclerosis), CC
CC neurological (e.g. epilepsy, Huntington's disease, stroke), CC
CC immune/inflammatory (e.g. AIDS, allergies) and developmental (e.g. CC
CC Hypothyroidism, Cushing's syndrome) disorders, or infections.
XX
XX
SQ Sequence 509 AA;
Query Match 77.7%; Score 1135; DB 8; Length 509;
Best Local Similarity 89.2%; Pred. No. 3.6e-111;
Matches 214; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
QY 41 QIQFADDMQEFTEPKTKGRSLRSISQSSTDSYSSAASYTSSDDEVSPPREKQOTNSK 100
DB 20 QIQFADQKOFENKRPFKIGRRSLRSISQSSTDSYSSAASYTSSDDETSPPRDKQOKNSK 79
QY 101 GSSNFCVKNIKQAEFRREIEIAEODMSALISLRKXQGEKPLAGAKIVGCTHITTAQTA 160
DB 80 GSSDFCVKNIKQAEFRREIEIAEODMPALMRKRAQGEKPLAGAKIVGCTHITTAQTA 139
QY 161 LIETTLGALGAOCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWMCIDRCVNMDG 220
DB 140 LMETLGLAGOCRMAACNIYSTLNEVAALAESEGFVFAWKGESEDDFWMCIDRCVNVEG 199
QY 221 WQANMILDDGGDLTHWVYKXYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANM 280
DB 200 WQNMILDDGGDLTHWVYKXYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANM 259

Search completed: September 6, 2006, 19:21:46
Job time : 111.174 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:22:08 ; Search time 18.5652 Seconds
(without alignments)
1451.138 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_280
Perfect score: 1461
Sequence: 1 MSMPDAMPPLPGVGEELKQAK.....RLYQLSKAGKLCVPMANVND 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1262	86.4	597	2 T08681	adenosylhomocystei
2	767	52.5	527	1 S01302	adenosylhomocystei
3	562	38.5	469	2 H83591	S-adenosyl-L-homoc
4	521.5	35.7	433	1 JC2480	adenosylhomocystei
5	520	35.6	433	2 T40763	adenosylhomocystei
6	511	35.0	449	2 S50546	adenosylhomocystei
7	509	34.8	430	1 A27655	adenosylhomocystei
8	503	34.4	432	1 A26583	adenosylhomocystei
9	502.5	34.4	432	2 T13218	adenosylhomocystei
10	499	34.2	437	1 A43629	adenosylhomocystei
11	477	32.6	437	1 A45569	adenosylhomocystei
12	471	30.2	485	2 S71621	adenosylhomocystei
13	434	29.7	485	2 T06764	adenosylhomocystei
14	433	29.6	466	2 AF2580	S-adenosylhomocyst
15	433	29.6	466	2 D97362	adenosylhomocystei
16	432	29.6	485	2 S18379	adenosylhomocystei
17	432	29.6	485	2 C71400	adenosylhomocystei
18	430.5	28.5	481	2 AG3505	adenosylhomocystei
19	430	28.4	495	2 B70593	adenosylhomocystei
20	425	28.1	462	1 A46035	adenosylhomocystei
21	425	28.1	492	2 D87005	adenosylhomocystei
22	418	28.6	463	2 H87280	probable S-adenosy
23	388.5	26.6	479	1 A54040	adenosylhomocystei
24	369.5	25.3	446	2 D82730	adenosylhomocystei
25	334.5	22.9	399	2 B72649	probable adenosylh
26	319.5	21.9	417	2 S58193	adenosylhomocystei
27	319.5	21.9	442	2 C90224	S-adenosyl-L-homoc
28	302	20.7	418	2 E70401	S-adenosylhomocyst
29	289.5	19.8	415	1 C64473	adenosylhomocystei

30	274.5	18.8	422	2 B75064	adenosylhomocystei
31	273	18.7	425	2 S75518	adenosylhomocystei
32	272.5	18.7	425	2 H71167	probable S-adenosy
33	265	18.1	425	2 AC1983	adenosylhomocystei
34	261.5	17.9	405	2 G69499	adenosylhomocystei
35	256.5	17.6	417	2 F69085	adenosylhomocystei
36	239.5	16.4	427	2 G84375	adenosylhomocystei
37	226.5	15.5	404	2 B72409	adenosylhomocystei
38	98.5	6.7	1328	2 AE2351	protoporphyrin IX
39	98	6.7	549	2 A12315	ribosomal large ch
40	97	6.6	269	2 I50504	nk2.2 protein - ze
41	96	6.6	1379	2 S37310	protoporphyrin IX
42	95.5	6.5	1087	2 T49496	hypothetical prote
43	95	6.5	414	2 A38205	nuclear localizati
44	94	6.4	1383	2 T07126	magnesium chelatas
45	93.5	6.4	599	2 T51548	hypothetical prote

ALIGNMENTS

RESULT 1					
T08681					
adenosylhomocysteinase (EC 3.3.1.1) DKFZP564A1523 - human (fragment)					
N.Alternate names: protein DKFZP564A1523.1					
C.Species: Homo sapiens (man)					
C.Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004					
C.Accession: T08681					
R.Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.					
submitted to the Protein Sequence Database, May 1999					
A.Reference number: Z16469					
A.Accession: T08681					
A.Molecule type: mRNA					
A.Residues: 1-597 <MAN>					
A.Cross-references: UNIPROT:Q9UG84; UNIPARC:UPI000006FAA4; EMBL:AL049954					
A.Experimental source: fetal brain; clone DKFZP564A1523					
C.Genetics:					
A.Note: DKFZP564A1523.1					
C.Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type					
C.Keywords: NAD; thioether hydrolase					
F.379-408/Region: beta-alpha-beta NAD nucleotide-binding fold					
F.244,278/Active site: Cys #status predicted					
Query Match	86.4%	Score 1262;	DB 2;	Length 597;	
Best Local Similarity	80.0%	Pred. No. 1.1e-95;			
Matches 252;	Conservative 8;	Mismatches 19;	Indels 36;	Gaps 4;	
QY	1 MSMPDAMPPLP-----GVGE---ELKQAKETIDAEKYSFMATVTKAPKK-----	40			
DB	34 ISQP-ALPLPQETQAPSGESENLRNLRQGRRAESSQNLISRLVSAQNGRSDPRWLMI	92			
QY	41 -----QIOFADDMOEFTEPPTKGRSLRSRSISQSTDSYSSAASYTDS	85			
DB	93 QLMPEIDSLSEISCFLOIOFADDMOEFTEPPTKGRSLRSRSISQSTDSYSSAASYTDS	152			
QY	86 DDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRIETIEQDMSALISLRKAAQGEKPLAG	145			
DB	153 DDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRIETIEQDMSALISLRKAAQGEKPLAG	212			
QY	146 AKIVGCHITNOTVLIETLCALGACRWASACNTYSTNEVAALAEAGVVFPAKGESE	205			
DB	213 AKIVGCHITNOTVLIETLCALGACRWASACNTYSTNEVAALAEAGVVFPAKGESE	272			
QY	206 DDFWMCIDRCVNMGMQAMILLDDGDLTHWVYKKYPNVFKKIRIGIVESYTGVRILYQL	265			
DB	273 DDFWMCIDRCVNMGMQAMILLDDGDLTHWVYKKYPNVFKKIRIGIVESYTGVRILYQL	332			
QY	266 SKAGKLCVPMANVND 280				
DB	333 SKAGKLCVPMANVND 347				
RESULT 2					

S01302
adenosylhomocysteinease (EC 3.3.1.1) - fruit fly (*Drosophila melanogaster*)
C/Species: *Drosophila melanogaster*
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S01302
R/Delorenzi, M.; Ali, N.; Saari, G.; Henry, C.; Wilcox, M.; Bienz, M.
EMBO J. 7, 3223-3231, 1988
A/Title: Evidence that the Abdominal-B element function is conferred by a trans-regula
A/Reference number: S01302; MUID:89030618; PMID:2903049
A/Accession: S01302
A/Molecule type: DNA
A/Residues: 1-527 <DEL>
A/Cross-references: UNIPROT:P50245; UNIPARC:UP10000168B0E; EMBL:X13168; NID:97675; PIDN:
C/Genetics:
A/Gene: FlyBase:Abd-B
A/Cross-references: FlyBase:FBgn0000015
A/Intons: 17/3; 41/1; 263/2; 369/3; 451/1
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
C/Keywords: NAD; thioether hydrolase
F/275-304/Region: beta-alpha-beta NAD nucleotide-binding fold
F/140,174/Active site: Cys #catalytic predicted

Query Match 52.5%; Score 767; DB 1; Length 527;

Best Local Similarity 66.1%; Pred. No. 3, 8e-55; Mismatches 41; Indels 2; Gaps 2;

Matches 144; Conservative 31; Mismatches 41; Indels 2; Gaps 2;

QY 64 SRSISQSTDSYSSAASYTDSDE-VSPREKQNTSKSSNFCVNIKQAEFRREIEI 122

DB 27 ARRFSDVSTCSFSTC-FTGSSDEEDVSPKDNHQRNSAGTDCVXSISKAFGRREIEI 65

QY 123 AEDMSALISLRKAGEKPLAKTIVGCHTITATVLETCALGACQRMACNIST 182

DB 86 ASSEMGIITLRRARDEKPLKANTVGCCHVNAQSIVLEALVQATVMAACNIST 145

QY 183 QNEVAALAEAGVAVFAWKESDEDFWMCIDRCVNDGMQANNILDDGDLTHVVKY 242

DB 146 QANVAALAEAGVAVFAWKESDEDFWMCIDRCVNDGMQANNILDDGDLTHVVKY 205

QY 243 NVFKIRGIVESVGVHRLYQSKAGKLCVPMANVND 280

DB 206 DYFKAIRGIVESVGVHRLYQSKAGKLCVPMANVND 243

RESULT 3

H83591
S-adenosyl-L-homocysteine hydrolase PA0432 (imported) - *Pseudomonas aeruginosa* (strain F

C/Species: *Pseudomonas aeruginosa*
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C/Accession: H83591
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mitzoguchi, S.D.; Warren, P.; Hickey, M.D.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000

A/Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: H83591
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-469 <STO>

A/Cross-references: UNIPROT:Q91685; UNIPARC:UP10000135502; GB:AE004480; GB:AE004091; NID

A/Experimental source: strain PA01
C/Genetics:
A/Gene: SAHH; PA0432
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type

Query Match 38.5%; Score 562; DB 2; Length 469;
Best Local Similarity 57.1%; Pred. No. 2, 2e-38; Mismatches 39; Indels 2; Gaps 1;
Matches 104; Conservative 37; Mismatches 39; Indels 2; Gaps 1;
QY 101 GSNFCVNIKQAEFRREIEIADQMSALISLRKAGEKPLAKTIVGCHTITATVLE 160
DB 9 GFTDYKAVDITLTAAGRREIIESEWPAIMGLRKRKAGQPLKAGKILGCHITITQTV 68

QY 161 LIETLCALGACQRMACNISTQNEVAALAEAGVAVFAWKESDEDFWMCIDRCVNDG 220

DB 69 LIETLVAALAEFRWSSCNIFSTQDAALAAAGVAVFAWKESDEDFWMCIDRCVNDG 128

QY 221 --WQANNILDDGDLTHVVKYKYPNVFKIRGIVESVGVHRLYQSKAGKLCVPMANV 278

DB 129 QPMANVNDGDLTHVVKYKYPNVFKIRGIVESVGVHRLYQSKAGKLCVPMANV 188

QY 279 ND 280

DB 189 ND 190

RESULT 4

UC2480
adenosylhomocysteinease (EC 3.3.1.1) - African clawed frog

N/Alternate names: S-adenosyl-L-homocysteine hydrolase
C/Species: *Xenopus laevis* (African clawed frog)
C/Date: 29-Mar-1995 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C/Accession: UC2480
R/Seery, L.T.; McCabe, B.D.; Schoenberg, D.R.; Whitehead, A.S.

Biochem. Biophys. Res. Commun. 205, 1539-1546, 1994
A/Title: S-Adenosyl-L-homocysteine hydrolase from *Xenopus laevis*. Identification, develop

A/Reference number: UC2480; MUID:95110290; PMID:7811234
A/Accession: UC2480
A/Molecule type: mRNA
A/Residues: 1-433 <SEE>

A/Cross-references: UNIPROT:P51893; UNIPARC:UP100001354E1; GB:L35559; NID:9558507; PIDN:
A/Experimental source: liver
C/Function:

A/Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adeno

C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type
C/Keywords: NAD; thioether hydrolase
F/215-244/Region: beta-alpha-beta NAD nucleotide-binding fold
F/79,113/Active site: Cys #catalytic predicted

Query Match 35.7%; Score 521.5; DB 1; Length 433;

Best Local Similarity 54.5%; Pred. No. 4, 3e-35; Mismatches 43; Indels 1; Gaps 1;

Matches 97; Conservative 37; Mismatches 43; Indels 1; Gaps 1;

QY 104 NFCVNIKQAEFRREIEIADQMSALISLRKAGEKPLAKTIVGCHTITATVLE 163

DB 6 SYKADISLADGKRAIEIAENEMPGIMKREHESKPLKARLAGCHMTITQTVLE 65

QY 164 TICALGACQRMACNISTQNEVAALAEAGVAVFAWKESDEDFWMCIDRCVNDG 222

DB 66 TITALGAEVQWSSCNIFSTQDAALAAAGVAVFAWKESDEDFWMCIDRCVNDG 125

QY 223 ANMILDDGDLTHVVKYKYPNVFKIRGIVESVGVHRLYQSKAGKLCVPMANVND 280

DB 126 LNMILDDGDLTHVVKYKYPNVFKIRGIVESVGVHRLYQSKAGKLCVPMANVND 183

RESULT 5

T40763
adenosylhomocysteinease - fission yeast (*Schizosaccharomyces pombe*)

C/Species: *Schizosaccharomyces pombe*
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: T40763
R/Lyne, M.; Rajandream, M.A.; Barrett, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.

submitted to the EMBL Data Library, March 1998
A/Reference number: Z21948
A/Accession: T40763
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-433 <LYN>
A/Cross-references: UNIPROT:O13639; UNIPARC:UP1000013550C; EMBL:AL022072; PIDN:CAA17833.3
A/Experimental source: strain 97zh-, cosmid c8D2
C/Genetics:
A/Gene: SPDB; SPBC8D2.18C
A/Map position: 2
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type

Query Match 35.6%; Score 520; DB 2; Length 433;
Best Local Similarity 55.2%; Pred. NO. 5.7e-35;
Matches 100; Conservative 33; Mismatches 46; Indels 2; Gaps 1;

102 SSNFCVKNIKOAEFGREIEIEAODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQAVL 161
3 TQNYKADISLAFAKGEIEIAENEMPGILAVREKAKAQPLKAGIACGLHMTITQAVL 62

162 ITTLCAAGACQMSACNIYSTONVAAALAEAGVAVPAMKGESEDDFWMCIDRCVNM--D 219
63 IETLVAGAEVWSSCNISTODHAAAIAATGVPAVFMKGETEEBEYLWCIEQOLSPFS 122

220 GQGANMILDDGGDLTTHVYKKNVFNFKIRGIVEESVTGVHRLYQSKXGKLCVPMANN 279
123 GEPILNLLDDGGDLTALVHERHPELLVDIRIGISEETTGHNLYKFKENKLVPAINNV 182

280 D 280
183 D 183

RESULT 6
S50546
adenosylhomocysteine (EC 3.3.1.1) - Yeast (*Saccharomyces cerevisiae*).
N:Alternate names: protein YER043C; S-adenosyl-L-homocysteine hydrolase
C:Species: *Saccharomyces cerevisiae*
C:Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
C:Accession: S50546
R:Dieckrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of *S. cerevisiae* cosmid 9379, 9581, and lambda clone 4678.
A:Reference number: S50432
A:Accession: S50546
A:Molecule type: DNA
A:Residues: 1-449 <DIE>
A:Cross-references: UNIPROT:P39954; UNIPARC:UP1000013551C; EMBL:U18796; NID:G603265; PDB
C:Genetics:
A:Gene: SGD:SAH1; MIPS:YER043C
A:Cross-references: SGD:S0000845; MIPS:YER043C
A:Map position: 5R
C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type
C:Keywords: NAD; thioether hydrolase
F:214-242/Region: beta-alpha-beta NAD nucleotide-binding fold
F:80.114/Active site: Cys #status predicted

Query Match 35.0%; Score 511; DB 2; Length 449;
Best Local Similarity 53.3%; Pred. No. 3.2e-34;
Matches 98; Conservative 36; Mismatches 48; Indels 2; Gaps 1;

99 SKGSSNFCVKNIKOAEFGREIEIEAODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQ 158
2 SAPAONNYKADISLAFAKGEIEIEAENEMPGILAVREKAKAQPLKAGIACGLHMTITQ 61

159 AVLIEFLCAGACQMSACNIYSTONVAAALAEAGVAVPAMKGESEDDFWMCIDRCVNM--CV 216
62 AVLIEFLCAGACQMSACNIYSTONVAAALAEAGVAVPAMKGESEDDFWMCIDRCVNM--CV 216

217 NMDGQANMILDDGGDLTTHVYKKNVFNFKIRGIVEESVTGVHRLYQSKXGKLCVPM 276
122 FQDNKKMLNLLDDGGDLTTLVHEKHEMLEDCGISEETTGHNLYKFKENKLVPAINNV 181

277 NVND 280
182 NVND 185

RESULT 7
A27655
adenosylhomocysteine (EC 3.3.1.1) - slime mold (*Dictyostelium discoideum*)
N:Alternate names: S-adenosyl-L-homocysteine hydrolase
C:Species: *Dictyostelium discoideum*
C:Date: 31-Mar-1989 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: A27655; S06394

R:Kasir, J.; Aksamit, R.R.; Backlund Jr., P.S.; Cantoni, G.L.
Biochem. Biophys. Res. Commun. 153, 359-364, 1988
A:Title: Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from *Dictyostelium* d
A:Reference number: A27655; MUID:88240426; PMID:3288206
A:Accession: A27655
A:Molecule type: mRNA
A:Residues: 1-430 <KAS>
A:Cross-references: UNIPROT:P10819; UNIPARC:UP100001354BE; GB:M19937; NID:g167663; PDB:
R:Gulton, M.C.; Part, D.; Veron, M.
Biochimie 70, 835-840, 1988
A:Title: Cloning of a cDNA for the S-adenosyl-L-homocysteine hydrolase from *Dictyostelium*
A:Reference number: S06394; MUID:89000991; PMID:3139100
A:Accession: S06394
A:Molecule type: mRNA
A:Residues: "VTKSSPMKPLHYQ", 270-311, 'G', 313-323, 'S', 325-359, 'SVTK', 365-382, 'P', 384-430
A:Cross-references: UNIPARC:UP100001689D; EMBL:X12523; NID:g7204; PDB:CAJ1040.1; PID:
A:Note: this sequence differs at the amino end by an apparent frame shift; comparison to
C:Function:
A:Description: catalyzes the reversible hydrolysis of S-adenosyl-L-homocysteine to adenos
C:Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAH type
C:Keywords: NAD; thioether hydrolase
F:213-242/Region: beta-alpha-beta NAD nucleotide-binding fold
F:78.112/Active site: Cys #status predicted

Query Match 34.8%; Score 509; DB 1; Length 430;
Best Local Similarity 54.8%; Pred. No. 4.5e-34;
Matches 97; Conservative 34; Mismatches 46; Indels 0; Gaps 0;

104 NECVKNIKOAEFGREIEIEAODMSALISLRKRAQGEKPLAGAKIVGCTHTTAQAVL 163
5 HKVADISLAAGKREIEIAENEMPGILAVREKAKAQPLKAGIACGLHMTITQAVL 64

164 ITLCAAGACQMSACNIYSTONVAAALAEAGVAVPAMKGESEDDFWMCIDRCVNDGQVA 223
65 TLTAAGQVOWSSCNISTODHAAAIAATGVPAVFMKGETEEBEYLWCIEQOLSPFS 124

224 NMILDDGGDLTTHVYKKNVFNFKIRGIVEESVTGVHRLYQSKXGKLCVPMANNVND 280
125 NMILDDGGDLTTLVHEKHEMLEDCGISEETTGHNLYKFKENKLVPAINNVND 181

RESULT 8
A26583
adenosylhomocysteine (EC 3.3.1.1) - rat
N:Alternate names: S-adenosyl-L-homocysteine hydrolase
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 19-Nov-1988 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: A26583; B26191; S69333
R:Ogawa, H.; Gomi, T.; Mueckler, M.M.; Fujioke, M.; Backlund Jr., P.S.; Aksamit, R.R.; U
Proc. Natl. Acad. Sci. U.S.A. 84, 719-723, 1987
A:Title: Amino acid sequence of S-adenosyl-L-homocysteine hydrolase from rat liver as de
A:Reference number: A26583; MUID:87118240; PMID:3027698
A:Accession: A26583
A:Molecule type: mRNA
A:Residues: 1-432 <OGA>
A:Cross-references: UNIPROT:P10760; UNIPARC:UP10000167A53; GB:M15185; NID:g202803; PDB:
R:Gomi, T.; Ogawa, H.; Fujioke, M.
J. Biol. Chem. 261, 13422-13425, 1986
A:Title: S-adenosylhomocysteine from rat liver. Amino acid sequences of the peptides c
A:Reference number: A92560; MUID:87008564; PMID:3759971
A:Accession: A26191
A:Molecule type: protein
A:Residues: 76-94 <GOM>
A:Cross-references: UNIPARC:UP10000172A00
A:Accession: B26191
A:Molecule type: protein
A:Residues: 104-121 <G02>
A:Cross-references: UNIPARC:UP10090172A00
A:Note: in a manner saturably inhibited by adenosine (a product) or adenine (a competit
-9 and Cys-113, suggesting a role for these residues at the active site; however, neith
R:Merla, A.; Aksamit, R.R.; Kasir, J.; Cantoni, G.L.
Eur. J. Biochem. 229, 575-582, 1995
A:Title: The gene and pseudogenes of rat S-adenosyl-L-homocysteine hydrolase.

C/Accession: AF2580
R/Wood, D.W.; Seubold, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, D.
erage, G.; Giller, W.; Grant, C.; Guenther, D.; Kuttyavin, T.; Levy, R.; Li, M.; Mclell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A/Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A/Reference number: AB25777; MUID:21608550; PMID:11743193
A/Accession: AF2580
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-466 <KUR>
A/Cross-references: UNIPROT:Q8UJ99, UNIPARC:UPI00001354E6, GB:AE008688, PIDN:AL41060.1;
A/Experimental source: strain C58 (Dupont)
C/Genetics:
A/Gene: ahcy
A/Map position: circular chromosome
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type

Query Match 29.6%; Score 433; DB 2; Length 466;
Best Local Similarity 44.1%; Pred. No. 8.6e-28;
Matches 94; Conservative 29; Mismatches 54; Indels 36; Gaps 3;

QY 104 NRCVKIKQAEFRREIEIEODMSALISLRKRAQGEKPLAGAKIVGCTHITQTAVLIE 163
DB 6 DYIVADINILAAFGKKEIDIAETEMPGIMSCRKESKPLKARITGSLMTIQTGLIE 65

QY 164 TLGALGACRMASCNISTYONEVAALAEAGVAFPAWKGESEDDFWWCIDRCVN-MDGMQ 222
DB 66 TLKELEGEIRFMAECNIFSTQDHAAALAAAGIPFAVKGESLTREWEYTDKIFQWTDGGL 125

QY 223 ANNILDDGGDLTHWV-----YKKYPNVFKK---- 247
DB 126 SNMILDDGGDATMYILLGARABAGEDVLSNPGSEEEELFPAQINKRLKASPGWFTKORDA 185

QY 248 IRGIVESTGVHRLYOLSKAGKLCVPANVND 280
DB 186 LKGVTETTTGVHRLYDLAKKGLPPPAIVND 218

RESULT 15
D97362
adenosylhomocysteine (S-adenosyl-L-homocysteine hydrolase) (adohcyase) [imported] - Ag
C/Species: *Agrobacterium tumefaciens*
C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C/Accession: D97362
R/Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Ouello, B.; Goldman,
A.; Liu, F.; Woliam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tum*
A/Reference number: A97359; MUID:21608551; PMID:11743194
A/Accession: D97362
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-466 <KUR>
A/Cross-references: UNIPROT:Q8UJ99, UNIPARC:UPI00001354E6, GB:AE007869, PIDN:AAK85853.1;
C/Genetics:
A/Gene: AGR C 46
A/Map position: circular chromosome
C/Superfamily: S-adenosyl-L-homocysteine hydrolase, human SAHH type

Query Match 29.6%; Score 433; DB 2; Length 466;
Best Local Similarity 44.1%; Pred. No. 8.6e-28;
Matches 94; Conservative 29; Mismatches 54; Indels 36; Gaps 3;

QY 104 NRCVKIKQAEFRREIEIEODMSALISLRKRAQGEKPLAGAKIVGCTHITQTAVLIE 163
DB 6 DYIVADINILAAFGKKEIDIAETEMPGIMSCRKESKPLKARITGSLMTIQTGLIE 65

QY 164 TLGALGACRMASCNISTYONEVAALAEAGVAFPAWKGESEDDFWWCIDRCVN-MDGMQ 222
DB 66 TLKELEGEIRFMAECNIFSTQDHAAALAAAGIPFAVKGESLTREWEYTDKIFQWTDGGL 125

QY 223 ANNILDDGGDLTHWV-----YKKYPNVFKK---- 247
DB 126 SNMILDDGGDATMYILLGARABAGEDVLSNPGSEEEELFPAQINKRLKASPGWFTKORDA 185

QY 248 IRGIVESTGVHRLYOLSKAGKLCVPANVND 280
DB 186 LKGVTETTTGVHRLYDLAKKGLPPPAIVND 218

Search completed: September 6, 2006, 19:30:47
Job time : 19.5652 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:15:48 ; Search time 143.348 Seconds
(without alignments)
1806.825 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_280
Perfect score: 1461
Sequence: 1 MSMPDAMPFVGVEELKQAK.....RLYQLSKAGKLCVPANMNVND 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1461	100.0	530	Q96PK4 HUMAN	Q96PK4 homo sapien
2	1461	100.0	530	Q80SWI MOUSE	Q80SWI mus musculu
3	1461	100.0	599	Q2FAJ6 HUMAN	Q2FAJ6 homo sapien
4	1461	100.0	607	Q502W8 HUMAN	Q502W8 homo sapien
5	1461	100.0	623	Q6P171 HUMAN	Q6P171 homo sapien
6	1389	95.1	540	Q5F3Q3 CHICK	Q5F3Q3 gallus gall
7	1307	89.5	500	Q43865 HUMAN	Q43865 homo sapien
8	1259	86.2	505	Q2NKH8 HUMAN	Q2NKH8 homo sapien
9	1228	84.1	484	Q9UG84 HUMAN	Q9UG84 homo sapien
10	1222	83.6	483	Q5VSM0 HUMAN	Q5VSM0 homo sapien
11	1195.5	81.8	554	Q49S42 BRARE	Q49S42 brachydanio
12	1195	81.8	520	Q6E1P1 XENLA	Q6E1P1 xenopus lae
13	1193	81.7	512	Q7R2B5 BRARE	Q7R2B5 brachydanio
14	1170	80.1	500	Q49S41 BRARE	Q49S41 brachydanio
15	1165	79.7	491	Q4RXQ1 TETNG	Q4RXQ1 tetradon n
16	1162	79.5	611	Q49S41 HUMAN	Q49S41 homo sapien
17	1160.5	79.4	588	Q5B143 XENTR	Q5B143 xenopus tro
18	1160	79.4	613	Q68F14 MOUSE	Q68F14 mus musculi
19	1158	79.3	585	Q4RYT5 TETNG	Q4RYT5 tetradon n
20	1154.5	79.0	588	Q6EEX1 XENLA	Q6EEX1 xenopus lae
21	1149	78.6	591	Q6PC06 BRARE	Q6PC06 brachydanio
22	1142	78.2	508	Q8B1H1 MOUSE	Q8B1H1 mus musculu
23	1140	78.0	508	Q5R889 PONPY	Q5R889 pongo pygma
24	1136	77.8	530	Q6ZNS6 HUMAN	Q6ZNS6 homo sapien
25	1122	76.8	583	Q6AZU3 XENLA	Q6AZU3 xenopus lae
26	1096.5	75.1	541	Q4RHJ7 TETNG	Q4RHJ7 tetradon n
27	984	67.4	478	Q80TQ9 MOUSE	Q80TQ9 mus musculu
28	847	58.0	521	Q6NR07 DROME	Q6NR07 drosophila
29	847	58.0	521	Q9VZX9 DROME	Q9VZX9 drosophila
30	772	52.8	492	Q43865 DROME	Q43865 drosophila
31	772	52	504	Q7KSG0 DROME	Q7KSG0 drosophila

32	757.5	51.8	522	2	Q5DH82 SCHJA	Q5dh82 schistosoma
33	707	48.4	432	2	Q7Q871 ANOGA	Q7q871 anopheles g
34	669	45.8	317	2	Q6ZMW9 HUMAN	Q6zwm9 homo sapien
35	609.5	41.7	499	2	Q4S7H8 TETNG	Q4s7h8 tetradon n
36	574	39.3	469	2	Q4J1U2 AZOVI	Q4j1u2 azotobacter
37	567.5	38.8	437	2	Q3J7R4 NITOC	Q3j7r4 nitrosococc
38	562	38.5	469	1	SAHH_PSEAE	Q91685 pseudomonas
39	560	38.3	467	1	SAHH_ACTAD	Q6fa43 actinobact
40	557	38.1	469	2	Q4Z292_PSEU2	Q4z292 pseudomonas
41	556	38.1	469	1	SAHH_PSEEM	Q87V73 pseudomonas
42	555	38.0	436	1	SAHH_LEPIC	Q75fue leptospira
43	555	38.0	436	1	SAHH_LEPIN	Q88xv1 leptospira
44	555	38.0	463	2	Q5SLT4_9C8AM	Q5slt4 hanelia che
45	554	37.9	469	2	Q48PB5_PSE14	Q48pb5 pseudomonas

ALIGNMENTS

```
RESULT 1
Q96PK4_HUMAN PRELIMINARY; PRT; 530 AA.
AC Q96PK4;
DT 01-DEC-2001, integrated into UniProtKB/TREMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-MAR-2006, entry version 25.
DE Adenosylhomocysteine hydrolase (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-
DE homocysteine hydrolase).
GN Name=AHCYL1; ORFNames=RP11-180N18.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21901265; PubMed=11904675; DOI=10.1007/s00251-001-0402-z;
RA Dekker J.W., Budhia S., Angel N.Z., Cooper B.J., Clark G.J.,
RA Hart D.N., Kato M.;
RT "Identification of an S-adenosylhomocysteine hydrolase-like transcript
RT induced during dendritic cell differentiation.";
RL Immunogenetics 53:993-1001(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Martin S.;
RP Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
CC homocysteine + adenosine.
CC -!- Cofactor: NAD (by similarity).
CC -!- Pathway: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC
EMBL AF315687; AAL26869.1; -; mRNA.
EMBL EMBL; AL772411; CAH70965.1; -; Genomic DNA.
HSSP; P10760; 1B3R.
DR Ensembl; ENSG00000168710; Homo sapiens.
DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR013321; Ad_hcy_hydrolase.
DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase; NAD; 1.
DR TIGRfam; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADOHCYASE_1; 1.
DR PROSITE; PS00739; ADOHCYASE_2; 1.
KW Hydrolase; NAD; One-carbon metabolism.
SQ SEQUENCE 530 AA; 58951 MW; 974D23361A245D04 CRC64;
```

Query Match 100.0%; Score 1461; DB 2; Length 530;
 Best Local Similarity 100.0%; Pred. No. 5,6e-108;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTTKAPKKQIQFADDMQEFKFPKTKR 60
 1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTTKAPKKQIQFADDMQEFKFPKTKR 60
 1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTTKAPKKQIQFADDMQEFKFPKTKR 60

61 RLSRSISGSSSTDSYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRI 120
 61 RLSRSISGSSSTDSYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRI 120
 61 RLSRSISGSSSTDSYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRI 120

121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLCALGAQCRWSACNIT 180
 121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLCALGAQCRWSACNIT 180
 121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLCALGAQCRWSACNIT 180

181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGGDLTHWVYKK 240
 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGGDLTHWVYKK 240
 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGGDLTHWVYKK 240

241 YPNVFKIRGIVEESYTGVRHLYQLSKAGKLCVPMANVND 280
 241 YPNVFKIRGIVEESYTGVRHLYQLSKAGKLCVPMANVND 280
 241 YPNVFKIRGIVEESYTGVRHLYQLSKAGKLCVPMANVND 280

RESULT 2
 080SW1 MOUSE PRELIMINARY; PRT; 530 AA.
 AC 080SW1; Integrated into UniProtKB/TrEMBL.
 DT 01-JUN-2003; sequence version 1.
 DT 01-JUN-2003; sequence version 1.
 DT 07-MAR-2006; entry version 26.
 DE S-adenosylhomocysteine hydrolase-like 1 (IP3R binding protein released with inositol 1,4,5-trisphosphate) (S-adenosylhomocysteine hydrolase-like protein).
 GN Name-Ahcy1; Synonyms=Irbt;
 OS Mus musculus (Mouse);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 [1]
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=Czech II; TISSUE=Mammary tumor metastasized to lung.
 RC MMTV-LTR/Mutl model. Expression driven by an MMTV-LTR enhancer.
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Piatige C., Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Millar S.J., Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodighiero S., Sanchez A., Blakesley R.C., Touchman J.W., Green E.D., Bouffard G.G., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywicki M.T., Skalska U., Smalins D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 NUCLEOTIDE SEQUENCE.
 RC STRAIN=Czech II; TISSUE=Mammary tumor metastasized to lung.
 RC MMTV-LTR/Mutl model. Expression driven by an MMTV-LTR enhancer.
 RG NIH MGC Project;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 RN

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Cerebellum;
 RA MEDLINE=22526701; PubMed=12525476; DOI=10.1074/jbc.M210119200;
 RX Ando H., Mizutani A., Matsura T., Mikoshiba K.;
 RT "IRBIT", a novel inositol 1,4,5-trisphosphate (IP3) receptor-binding protein, is released from the IP3 receptor upon IP3 binding to the receptor.";
 RT J. Biol. Chem. 278:10602-10612(2003).
 [4]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=21901265; PubMed=11904675; DOI=10.1007/s00251-001-0402-z;
 RA Dekker J.W., Budhia S., Angel N.Z., Cooper B.J., Clark G.J., Hart D.N., Kato M.;
 RT Identification of an S-adenosylhomocysteine hydrolase-like transcript induced during dendritic cell differentiation.";
 RT Immunogenetics 53:993-1001(2002).
 CC -1 MISCELLANEOUS: The sequence shown here is derived from an EMBL/GenBank/DBJ third party annotation (TPA) entry.
 CC -1 CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-homocysteine + adenosine.
 CC -1 COFACTOR: NAD (By similarity).
 CC -1 PATHWAY: Activated methyl cycle.
 CC -1 SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs license

EMBL; BC018218; AAH18218.2; -; mRNA.
 EMBL; AB092504; BAC65166.1; -; mRNA.
 EMBL; BK000547; DAA00059.1; -; mRNA.
 HSSP; P10760; 1B3R.
 DR Ensembl; ENSMUSG0000027893; Mus musculus.
 DR MGI; MGI:2385184; Ahcy1.
 DR GO; GO:0004013; F:adenosylhomocysteine activity; RCA.
 DR GO; GO:0016787; F:hydrolase activity; RCA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; RCA.
 DR InterPro; IPR000043; Ad_hcy_hydrolase.
 DR InterPro; IPR013321; Arc_rbn_hlx.
 DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam; PF05221; AdhCysase; 1.
 DR Pfam; PF0670; AdhCysase; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00739; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 KW Hydrolase; NAD; One-carbon metabolism.
 SQ SEQUENCE 530 AA; 58951 MW; 974D23361A245D04 CRC64;

Query Match 100.0%; Score 1461; DB 2; Length 530;
 Best Local Similarity 100.0%; Pred. No. 5,6e-108;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTTKAPKKQIQFADDMQEFKFPKTKR 60
 1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTTKAPKKQIQFADDMQEFKFPKTKR 60
 1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTTKAPKKQIQFADDMQEFKFPKTKR 60

61 RLSRSISGSSSTDSYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRI 120
 61 RLSRSISGSSSTDSYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRI 120
 61 RLSRSISGSSSTDSYSSAASYTSSDDEVSPEKQOTNSKGSNFCVKNIKQAEFGRRRI 120

121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLCALGAQCRWSACNIT 180
 121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLCALGAQCRWSACNIT 180
 121 EIAEQDMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLCALGAQCRWSACNIT 180

181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGGDLTHWVYKK 240
 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGGDLTHWVYKK 240
 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNDGQANMILDDGGDLTHWVYKK 240

241 YPNVFKIRGIVEESYTGVRHLYQLSKAGKLCVPMANVND 280
 241 YPNVFKIRGIVEESYTGVRHLYQLSKAGKLCVPMANVND 280
 241 YPNVFKIRGIVEESYTGVRHLYQLSKAGKLCVPMANVND 280

RESULT 3

Q2TAJ6 HUMAN
ID Q2TAJ6 HUMAN PRELIMINARY; PRT; 599 AA.
AC Q2TAJ6
DT 24-JAN-2006, integrated into UniProtKB/TrEMBL.
DT 24-JAN-2006, sequence version 1.
DT 07-MAR-2006, entry version 3.
DE AHCYL1 protein (Fragment).
GN Name=AHCYL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheef C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RG NIH MGC Project;
RX Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- COFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license

CC EMBL; BC110896; AA110897.1; -; mRNA.
CC Hydrolyase; NAD; One-carbon metabolism.
FT NON TER 1
SQ SEQUENCE 599 AA; 65700 MW; C85BAEB1950CEAAB CRC64;
Query Match 100.0%; Score 1461; DB 2; Length 599;
Best Local Similarity 100.0%; Pred. No. 6.5e-108;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 250 STONEVAAAALAEAGVAVFAWKGESEDDFWWCICDRVCMNDGQAMNILLDDGGDLTHWVYKK 309
Qy 241 YPNVEFKIRGIVESVTVGVHRLYQLSKAGKLCVPMANVND 280
Db 310 YPNVEFKIRGIVESVTVGVHRLYQLSKAGKLCVPMANVND 349
RESULT 4
Q502W8 HUMAN
ID Q502W8 HUMAN PRELIMINARY; PRT; 607 AA.
AC Q502W8;
DT 07-JUN-2005, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Scheef C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RX Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
homocysteine + adenosine.
CC -1- COFACTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license

CC EMBL; BC095476; AA095476.1; -; mRNA.
CC EMBL; ENSG00000168710; Homo sapiens.
CC GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
CC GO; GO:0016787; F:hydrolyase activity; IEA.
CC GO; GO:0006730; P:one-carbon compound metabolism; IEA.
CC InterPro; IPR000043; Ad hcy hydrolyase.
CC InterPro; IPR013321; Arc_rhn_hlx_hlx.
CC InterPro; IPR011281; Cytochrome_B450.
CC PANTHER; PTHR11784; Ad_hcy_hydrolyase; 1.
CC Pfam; PF05221; AdoHcyase; 1.
CC Pfam; PF00670; AdoHcyase_NAD; 1.
CC TIGRFAMs; TIGR00936; ahcy; 1.
CC PROSITE; PS00738; ADOHCYASE_1; 1.
CC PROSITE; PS00739; ADOHCYASE_2; UNKNOWN_1.

DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
 KW Hydroxylase; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON_TER 1 1
 SQ SEQUENCE 607 AA; 66683 MW; 349412833E2D5911 CRC64;
 Query Match 100.0%; Score 1461; DB 2; Length 607;
 Best Local Similarity 100.0%; Pred. No. 6.6e-108;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 60
 DB 78 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 137
 QY 61 RLSRSISQSSSTDSYSSAASYTSSDDEVSPPREKQOTNSKGSNFCVKNIKQAEFRREI 120
 DB 138 RLSRSISQSSSTDSYSSAASYTSSDDEVSPPREKQOTNSKGSNFCVKNIKQAEFRREI 197
 QY 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHITQTAVLIETLCALGAQCRWSACNIT 180
 DB 198 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHITQTAVLIETLCALGAQCRWSACNIT 257
 QY 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDSQANMILDDGGDLTHWVYKX 240
 DB 258 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDSQANMILDDGGDLTHWVYKX 317
 QY 241 YPNVFKIRGIYVESVTGVHRLYQLSKAGKLCVPMANVND 280
 DB 318 YPNVFKIRGIYVESVTGVHRLYQLSKAGKLCVPMANVND 357

RESULT 5
 ID Q6P171 HUMAN PRELIMINARY; PRT; 623 AA.
 AC Q6P171;
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
 DT 05-JUL-2004, sequence version 1.
 DT 07-FEB-2006, entry version 13.
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh T.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughran N.A., Peters G.J., Abramson R.D., Mullen S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16699-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RA Strausberg R.;
 CC Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -i- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-

CC homocysteine + adenosine.
 CC -i- COFACTOR: NAD (By similarity).
 CC -i- PATHWAY: Activated methyl cycle.
 CC -i- SIMILARITY: Belongs to the adenosylhomocysteine family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC -----
 DR EMBL; BC065254; AA65254.1; -, mRNA.
 DR HSSP; P10760; I83R.
 DR Ensembl; ENSG00000168710; Homo sapiens.
 DR GO; GO:0004013; F:adenosylhomocysteine activity; IEA.
 DR GO; GO:0016787; F:hydroxylase activity; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad_hcy_hydroxylase.
 DR InterPro; IPR013321; Arc_xdh_hlx_hlx.
 DR InterPro; IPR01128; Cytochrome P450.
 DR PANTHER; PTHR11784; Ad_hcy_hydroxylase; 1.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF0670; AdoHcyase; 1.
 DR TIGRfam; TIGR00936; ahd; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 DR PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
 KW Hydroxylase; Hypothetical protein; NAD; One-carbon metabolism.
 FT NON_TER 1 1
 SQ SEQUENCE 623 AA; 68648 MW; B0A40ED58BAF3F23 CRC64;
 Query Match 100.0%; Score 1461; DB 2; Length 623;
 Best Local Similarity 100.0%; Pred. No. 6.6e-108;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 60
 DB 94 MSMPDMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 153
 QY 61 RLSRSISQSSSTDSYSSAASYTSSDDEVSPPREKQOTNSKGSNFCVKNIKQAEFRREI 120
 DB 154 RLSRSISQSSSTDSYSSAASYTSSDDEVSPPREKQOTNSKGSNFCVKNIKQAEFRREI 213
 QY 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHITQTAVLIETLCALGAQCRWSACNIT 180
 DB 214 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHITQTAVLIETLCALGAQCRWSACNIT 273
 QY 181 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDSQANMILDDGGDLTHWVYKX 240
 DB 274 STONEVAALAEAGVAVFAWKGESEDDFWWCIDRCVNMDSQANMILDDGGDLTHWVYKX 333
 QY 241 YPNVFKIRGIYVESVTGVHRLYQLSKAGKLCVPMANVND 280
 DB 334 YPNVFKIRGIYVESVTGVHRLYQLSKAGKLCVPMANVND 373

RESULT 6
 ID Q5F303 CHICK PRELIMINARY; PRT; 540 AA.
 AC Q5F303;
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Hypothetical protein.
 GN ORFNames=RCMB04.10b17;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;
 RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
 RA Fiedler P., Kutter S., Blagodatiski Y., Kostovska D., Koter M.,
 RA Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.,

"Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis."
Genome Biol. 6:R6-R6(2005).
-1- SIMILARITY: Belongs to the adenosylhomocysteine family.

CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs license

DR EMBL: AJ851597; CAH65231.1; -, mRNA.
DR GO: GO:0004013; F:adenosylhomocysteine activity; IEA.
DR GO: GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro: IPR000043; Ad_hcy_hydrolyase.
DR InterPro: IPR013321; Arg_rbm_hlx_hlx.
DR PANTHER: PTHR11784; Ad_hcy_hydrolyase; 1.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF00670; AdoHcyase_NAD; 1.
DR PROSITE: PS00738; ADOHCYASE_1; 1.
DR PROSITE: PS00739; ADOHCYASE_2; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 540 AA; 59231 MW; 66E479BFA2368F92 CRC64;

Query Match 95.1%; Score 1389; DB 2; Length 540;
Best Local Similarity 95.4%; Pred. No. 3,2e-102;
Matches 267; Conservative 5; Mismatches 4; Indels 4; Gaps 1;

QY 1 MSMPDAMPPLPGGEEELKQAKETEDAEKYSFMAVTYKAPKKOIOFADDMOEFTRPKTKR 60
DB 1 MSVP----PAGEEEKQKAEADAEKESFPMVTVKAPKKOIOFADDMOEFTRPKTKR 56
QY 61 RLSRSISQSSSTDSYSSAASYTSSDDEVSPEKQOTNSKSSNFCVKNIKOAEFGREI 120
DB 57 RLSLSISQSSSTDSYSSAASYTSSDDEVSPEKQOTNSKSSNFCVKNIKOAEFGREI 116
QY 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHTTQTAVALIETLCALGACRWSACNLY 180
DB 117 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHTTQTAVALIETLCALGACRWSACNLY 176
QY 181 STONVAAALAEAGVAFPMKGESEDDFWWCIDRCNMGMQANMLDDGGLTHVYVK 240
DB 177 STONVAAALAEAGVAFPMKGESEDDFWWCIDRCNMGMQANMLDDGGLTHVYVK 236
QY 241 YPNVEFKIRGIVESVTGVHRLYQLSKAGKLCVPMANVND 280
DB 237 YPNVEFKIRGIVESVTGVHRLYQLSKAGKLCVPMANVND 276

RESULT 7
SAHR2 HUMAN STANDARD; PRT; 500 AA.
ID SAHR2 HUMAN STANDARD; PRT; 500 AA.
AC 043865;
DT 15-DEC-1998, integrated into UniProtKB/Swiss-Prot.
DT 01-JUN-1998, sequence version 1.
DT 07-MAR-2006, entry version 44.
DT Putative adenosylhomocysteine 2 (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase).
DE Name=ACYL1; Synonyms=XPKONA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RN NUCLEOTIDE SEQUENCE (mRNA).
RP TISSUE=Skin;
RA Volpe J.P.G., McDowell M., Jostes R.F., Afzal V., Sadiński W., Tisek B.J., Legerstee R., Cleaver J.B.;
RT "Complementation of chromosomal instability in the xeroderma pigmentosum variant by a gene on human chromosome 1 with homology to S-adenosyl homocysteine hydrolase";
RT Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL (2)
RN NUCLEOTIDE SEQUENCE (LARGE SCALE MRNA).
RP TISSUE=Colon, and Placenta;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stalcup E., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., Mowen P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W., Villalón D.K., Munz D.M., Sodergren E.U., Lu X., Gibbs R.A., Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez R.W., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-homocysteine + adenosine.
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteine family.
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NoDerivs license

DR EMBL: U82761; AAC01960.1; -, mRNA.
DR EMBL: BC007576; AAH07576.1; -, mRNA.
DR EMBL: BC010681; AAH10681.1; -, mRNA.
DR EMBL: BC016942; AAH16942.1; -, mRNA.
DR HSSP: P10760; 1B3R.
DR Ensembl: ENSG00000168710; Homo sapiens.
DR HGNC: HGNC:344; AHCYL1.
DR MIM: 607826; gene.
DR InterPro: IPR000043; Ad_hcy_hydrolyase.
DR InterPro: IPR013321; Arg_rbm_hlx_hlx.
DR PANTHER: PTHR11784; Ad_hcy_hydrolyase; 1.
DR Pfam: PF05221; AdoHcyase; 1.
DR Pfam: PF00670; AdoHcyase_NAD; 1.
DR TIGRfam: TIGR00936; ahcy; 1.
DR PROSITE: PS00738; ADOHCYASE_1; 1.
DR PROSITE: PS00739; ADOHCYASE_2; 1.
DR KW Hydrolyase; NAD; One-carbon metabolism.
KW Putative adenosylhomocysteine 2.
FT FT 1 500
FT CHAIN 1
FT REGION 251 418 NAD binding (By similarity).
FT BINDING 125 125 Substrate (By similarity).
FT BINDING 199 199 Substrate (By similarity).
FT BINDING 224 224 Substrate (By similarity).
FT BINDING 254 254 Substrate (By similarity).
FT BINDING 258 258 Substrate (By similarity).
SQ SEQUENCE 500 AA; 55628 MW; FDEABEC70044B9DA CRC64;

Query Match 89.5%; Score 1307; DB 1; Length 500;
Best Local Similarity 100.0%; Pred. No. 1e-95;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 MATYTKAPKKOIOFADDMOEFTRPKTKGRSLRSISQSSSTDSYSSAASYTSSDDEVS 90
DB 1 MATYTKAPKKOIOFADDMOEFTRPKTKGRSLRSISQSSSTDSYSSAASYTSSDDEVS 60
QY 91 PREKOOTNSKSSNFCVKNIKOAEFGREIFIAODMSALISLRKRAQGEKPLAGAKIVG 150
DB 61 PREKOOTNSKSSNFCVKNIKOAEFGREIFIAODMSALISLRKRAQGEKPLAGAKIVG 120
QY 151 CTHITTAQTAVALIETLCALGACRWSACNLYSTONVAAALAEAGVAFPMKGESEDDFW 210
DB 121 CTHITTAQTAVALIETLCALGACRWSACNLYSTONVAAALAEAGVAFPMKGESEDDFW 180

```
QY 211 CIDRCVNMDSQANMILDDGGDLTHWYKYPNVFKKIRGIVEESVTGVRHLVQLSKAGK 270
DB 181 CIDRCVNMDSQANMILDDGGDLTHWYKYPNVFKKIRGIVEESVTGVRHLVQLSKAGK 240
QY 271 LCVPMANNVND 280
DB 241 LCVPMANNVND 250

RESULT 8
Q2NKM8 HUMAN
ID Q2NKM8 HUMAN PRELIMINARY; PRT; 505 AA.
AC Q2NKM8;
DT 07-FEB-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, sequence version 1.
DE AHCTYL1 protein (Fragment).
GN Name=AHCTYL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schlier G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loggellano N.A., Peters G.U., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Alakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (DEC-2005) to the EMBL/GenBank/DBJ databases.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
EMBL: BC11563; AAI11564.1; -; mRNA.
FT NON TER 1
SQ SEQUENCE 505 AA; 56469 MW; 0231B614A22D5662 CRC64;

Query Match 86.2%; Score 1259; DB 2; Length 505;
Best Local Similarity 99.6%; Pred. No. 7.3e-92;
Matches 240; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
DB 135 VLIETLCALGAOCRMSACNIYSTONEVAALAEAGVAVFAMKGESEDDFWWCIDRCVNMND 194
QY 220 GWOANMILDDGGDLTHWYKYPNVFKKIRGIVEESVTGVRHLVQLSKAGKLCVPMANNV 279
DB 195 GWOANMILDDGGDLTHWYKYPNVFKKIRGIVEESVTGVRHLVQLSKAGKLCVPMANNV 254
QY 280 D 280
DB 255 D 255

RESULT 9
Q9UG84 HUMAN
ID Q9UG84 HUMAN PRELIMINARY; PRT; 484 AA.
AC Q9UG84;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 2.
DE Adenosylhomocysteinease (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-
DE homocysteine hydrolase) (Fragment).
GN Name=DXF2P564A1523;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RG The German cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-
CC homocysteine + adenosine.
CC -1- CORRECTOR: NAD (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
EMBL: AL049954; CAB43223.2; -; mRNA.
DR PIR; T08681; T08681.
DR Ensembl; ENSG00000168710; Homo sapiens.
DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:006730; F:one-carbon compound metabolism; IEA.
DR INTERPRO; IPR000043; Ad_hcy_hydrolase.
DR PANTHER; PTHR11784; Ad_hcy_hydrolase; 1.
DR Pfam; PF05221; AdoHcyase; 1.
DR Pfam; PF00670; AdoHcyase; 1.
DR TIGRPFAM; TIGR00936; ahcy; 1.
DR PROSITE; PS00738; ADHOCYASE_1; 1.
DR PROSITE; PS00739; ADHOCYASE_2; 1.
DR KEGG; K01156; Hypothetical protein; NAD; One-carbon metabolism.
FT NON TER 1
SQ SEQUENCE 484 AA; 53869 MW; 8A55EF564F6B7E1D CRC64;

Query Match 84.1%; Score 1228; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 2.1e-89;
Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

DB 121 ALGACRMSACITISTONEVPAALAEAGVAFAMKGESEDDPWMCIDRCVNMGMQANMIL 180
 QY 227 LDDGDLTHWVYKYPNVFKIRGIVEESVTGVRHLYOLSKAGKLCVPAMNVND 280
 DB 181 LDDGDLTHWVYKYPNVFKIRGIVEESVTGVRHLYOLSKAGKLCVPAMNVND 234

RESULT 10

OSVSMO HUMAN PRELIMINARY; PRT; 483 AA.
 ID OSVSMO HUMAN
 AC OSVSMO
 DT 07-DEC-2004, integrated into UniProtKB/TrEMBL.
 DT 07-DEC-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE Adenosylhomocysteinease (EC 3.3.1.1) (AdoHcyase) (S-adenosyl-L-homocysteine hydrolase).
 GN Name=AHCYL1; ORFNames=Rp11-180N18.1-002;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Martin S.;
 CC Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-homocysteine + adenosine.
 CC -1- COFACTOR: NAD (By similarity).
 CC -1- PATHWAY: Activated methyl cycle.
 CC -1- SIMILARITY: Belongs to the adenosylhomocysteinease family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC EMBL; AL772411; CAH70966.1; -; Genomic DNA.
 DR Ensembl; ENSG00000168710; Homo sapiens.
 DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad hcy hydrolase.
 DR PANTHER; PTHR11784; Ad hcy hydrolase; 1.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF00670; AdoHcyase_NAD; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; 1.
 KM Hydrolase; NAD; One-carbon metabolism.
 SQ SEQUENCE 483 AA; 53753 MW; 18DFC7E74697E1D4 CRC64;

Query Match 83.6%; Score 1222; DB 2; Length 483;
 Best Local Similarity 100.0%; Pred. No. 6,2e-89;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 MOEFKTPFKTGRSLRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCV 107
 DB 1 MOEFKTPFKTGRSLRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCV 60
 QY 108 KNKKAEGRRRIETAEQMSALISLRKAQGEKPLAGAKITGCHITQTAVILETTCA 167
 DB 61 KNKKAEGRRRIETAEQMSALISLRKAQGEKPLAGAKITGCHITQTAVILETTCA 120
 QY 168 LGAOCRMSACNISTYSTONEVPAALAEAGVAFAMKGESEDDPWMCIDRCVNMGMQANMIL 227
 DB 121 LGAOCRMSACNISTYSTONEVPAALAEAGVAFAMKGESEDDPWMCIDRCVNMGMQANMIL 180
 QY 228 DDGDLTHWVYKYPNVFKIRGIVEESVTGVRHLYOLSKAGKLCVPAMNVND 280
 DB 181 DDGDLTHWVYKYPNVFKIRGIVEESVTGVRHLYOLSKAGKLCVPAMNVND 233

RESULT 11

O49S42_BRARE
 ID O49S42_BRARE PRELIMINARY; PRT; 554 AA.
 AC O49S42;
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE S-adenosylhomocysteine hydrolase-like protein variant 1.
 GN Name=ahcy11;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Cooper B.J., Key B., Carter A., Angel N.Z., Jackson A., Hart D.N.J., Kato M.;
 CC "Ectopic expression of adenosylhomocysteine hydrolase-like protein 1 (AHCYL1) causes dorsalization of zebrafish embryos: Zebrafish AHCYL1 cloning, gene structure and function";
 RT Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NonDerivs License
 CC EMBL; AY611473; AAU20792.1; -; mRNA.
 DR ZFIN; ZDB-GENE-021206-7; ahcy11.
 DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad hcy hydrolase.
 DR Pfam; PF05221; AdoHcyase; 1.
 DR Pfam; PF00670; AdoHcyase_NAD; 1.
 DR TIGRFAMs; TIGR00936; ahcy; 1.
 DR PROSITE; PS00738; ADOHCYASE_1; 1.
 DR PROSITE; PS00739; ADOHCYASE_2; UNKNOWN_1.
 KM Hydrolase.
 SQ SEQUENCE 554 AA; 61406 MW; 4E5F03E1D238BA36 CRC64;

Query Match 81.8%; Score 1195.5; DB 2; Length 554;
 Best Local Similarity 82.2%; Pred. No. 9.7e-87;
 Matches 236; Conservative 12; Mismatches 16; Indels 23; Gaps 3;

QY 17 KQAKIED-ARKYS-----FMATVTKAPKKQIOFA--DMQGEFTK 53
 DB 18 KEFKESENVARKYSAMTKRSGDVNMNVGELSAFTAVPTKSVKIKIFANQEDKQEFK 77
 QY 54 FPKTGRSLRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCVANKIKQ 113
 DB 78 FPKTGRSLRSISQSSSTDSYSSAASYTDSDEVSPEKQQTNSKSSNFCVANKIKQ 137
 QY 114 EFRREIRIADQMSALISLRKAQGEKPLAGAKITGCHITQTAVILETTCA 173
 DB 138 EFRREIRIADQMSALISLRKAQGEKPLAGAKITGCHITQTAVILETTCA 197
 QY 174 WSACNISTYSTONEVPAALAEAGVAFAMKGESEDDPWMCIDRCVNMGMQANMILDDGDL 233
 DB 198 WTACNISTYSTONEVPAALAEAGVAFAMKGESEDDPWMCIDRCVNMGMQANMILDDGDL 257
 QY 234 THWVYKYPNVFKIRGIVEESVTGVRHLYOLSKAGKLCVPAMNVND 280
 DB 258 THWVYKYPNVFKIRGIVEESVTGVRHLYOLSKAGKLCVPAMNVND 304

RESULT 12

O661P1_XENLA
 ID O661P1_XENLA PRELIMINARY; PRT; 520 AA.
 AC O661P1;
 DT 11-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 11-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 12.
 DE MGC6404 protein.
 GN Name=MGC6404;

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxId=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsuna K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC Klein S., Gerhard D.S.;
 RL Submitted (Aug-2004) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 CC EMBL: BC081269; AAH81269.1; -; mRNA.
 DR GO:0004013; Fadenosylhomocysteine activity; IEA.
 DR GO:0006730; Pione-carbon compound metabolism; IEA.
 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase; NAD; 1.
 DR TIGRfam: TIGR00936; ahcy; 1.
 DR PROSITE: PS00738; ADOHCYASE_1; 1.
 DR PROSITE: PS00739; ADOHCYASE_2; 1.
 SQ SEQUENCE 520 AA; 57839 MW; C73583CF180234C3 CRC64;

Query Match 81.8%; Score 1195; DB 2; Length 520;
 Best Local Similarity 82.6%; Pred. No. 9.8e-87;
 Matches 222; Conservative 18; Mismatches 19; Indels 12; Gaps 3;

QY 1 MSNPDAAPLPGVGEELKQAKIEBDAKYSFMTATVTKAPKKQIOPADMOEFYFPTKGR 60
 DB 1 MSLEPAV-----TTDEPAAEKFLPMAPVSKPKK-IQPADMOEFKFRRTKGR 49
 QY 61 RSLSRISISQSTSTSYSSASTYTSSSPDEVSPPKQOTNSGSSNFCVKNIKQAEFRRET 120
 DB 50 RSLSRISISQSTSTSYSSASTYTSSSPDEVSPPKQOTNSGSSNFCVKNIKQAEFRRET 109
 QY 121 EIAEQMSALISLRKAGEKPLAGAKIVGCTHITQTAVLITLALGACQMSACNIT 180
 DB 121 EIAEQMSALISLRKAGEKPLAGAKIVGCTHITQTAVLITLALGACQMSACNIT 180

DB 110 DIAEQMSALISLRKAGEKPLAGAKIVGCTHITQTAVLITLALGACQMSACNIT 169
 QY 181 STONEVAALAAAGVAVFAMKGESEDDFWWCIDRCVNMD-GQANNTLDDGDLTHWYK 239
 DB 170 STONEVAALAAAGVAVFAMKGESEDDFWWCIDRCVNADSGQANNIIDDGDLTHWYK 229
 QY 240 KYPNVFKIRGIVESYGVHLYQLSKAGKLCVPMANVD 280
 DB 230 KYPNVFKIRGIVESYGVHLYQLSKAGKLCVPMANVD 270

RESULT 13
 Q72B5_BRARE
 ID Q72B5_BRARE PRELIMINARY; PRT; 512 AA.
 AC Q72B5;
 DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
 DT 01-OCT-2003, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE S-adenosylhomocysteine hydrolase-like 1.
 GN Name=ahcy1;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxId=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Matsuna K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Umed T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Bosak S.A., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Kidney;
 RC Strausberg R.;
 RL Submitted (Jul-2003) to the EMBL/GenBank/DBJ databases.
 CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
 CC Distributed under the Creative Commons Attribution-NonDerivs license
 CC
 CC EMBL: BC054614; AAH54614.1; -; mRNA.
 DR HSSP: P10760; 1B3R.
 DR ZFIN: ZDB-GENE-021206-7; ahcy1.
 DR GO:0004013; Fadenosylhomocysteine activity; IEA.
 DR GO:0016787; F-hydrolase activity; IEA.
 DR GO:0006730; Pione-carbon compound metabolism; IEA.
 DR InterPro: IPR000043; Ad_hcy_hydrolase.
 DR PANTHER: PTHR11784; Ad_hcy_hydrolase; 1.
 DR Pfam: PF05221; AdoHcyase; 1.
 DR Pfam: PF00670; AdoHcyase; NAD; 1.
 DR TIGRfam: TIGR00936; ahcy; 1.
 DR PROSITE: PS00738; ADOHCYASE_1; 1.
 DR PROSITE: PS00739; ADOHCYASE_2; 1.
 DR HydroLase.
 SQ SEQUENCE 512 AA; 56776 MW; 3E0A09DFFE086683 CRC64;

Query Match Similarity	81.7%	Score 1193	DB 2	Length 512
Best Local Similarity	89.8%	Pred. No. 1.4e-86		
Matches 228	Conservative 11	Mismatches 13	Indels 2	Gaps 1
Qy	29	SPMATVTAPKPKQLOFA--DDMOEFTKPTPTKTGRSLRSISOSSTDSYSSAASYTSSD	86	
Db	9	AFTAVPTKHSVKKIQIPANOEDKQEFSPKPTKTGRSLRSISOSSTDSYSSAASYTSSD	68	
Qy	87	DEVSFRRQOTNSKSSSNFCVKNVIOAEFGREIEIEAEDMSALISLRPAQEKPLAA	146	
Db	69	DETSPREKSOVNSKSSDFCVKNVIOAEFGREIEIEAEDMSALISLRPAQEKPLAA	128	
Qy	147	KIVGTHITTAQTAVLIEITLCAAGCRMSACNIYSTONEVAALAEAGVAFAMGCESD	206	
Db	129	KVAGCTHITTAQTAVLIEITLCAAGCRMTACNIYSTONEVAALAEAGVAFAMGCESD	188	
Qy	207	DFMWCIDRCVNMDSQANMILDDGDLTHVYKKYPNVEFKIRGIYESVTGVRHLYOLS	266	
Db	189	DFMWCIDRCVNMDSQANMILDDGDLTHVYKKYPSVFKVRGIVYESVTGVRHLYOLS	248	
Qy	267	KAGKLCVPMNVND 280		
Db	249	KAGKLCVPMNVND 262		
RESULT 14				
Q49541_BRAE PRELIMINARY, PRT, 500 AA.				
ID	Q49541	BRARE	PRELIMINARY,	PRT, 500 AA.
AC	Q49541			
DT	13-SEP-2005		integrated into UniProtKB/TrEMBL.	
DT	13-SEP-2005		sequence version 1.	
DT	07-FEB-2006		entry version 2.	
DE	S-adenosylhomocysteine hydrolase-like protein variant 2.			
GN	Name=ancyl1;			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxId=7955;			
RN	[1]			
RP	NCBIELECTIDE SEQUENCE.			
RA	Cooper B.J., Key B., Carter A., Angel N.Z., Jackson A., Hart D.N.J.,			
RA	Kato M.;			
RT	"Ectopic expression of adenosylhomocysteine hydrolase-like protein 1			
RT	(ANCYL1) causes doralization of zebrafish embryos: Zebrafish ANCYL1			
RT	cloning, gene structure and function."			
RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NonDerivs License			
CC				
DR	EMBL; AY611474; AAU20793.1; -, mRNA.			
DR	ZFIN; ZDB-GENE-021206-7; ancyl1.			
DR	GO; GO:0004013; F:adenosylhomocysteine hydrolase activity; IEA.			
DR	GO; GO:0016787; F:hydrolase activity; IEA.			
DR	GO; GO:0006730; P:one-carbon compound metabolism; IEA.			
DR	InterPro; IPR000043; Ad_hcy_hydrolase.			
DR	Pfam; PF05221; AdoHcyase; 1.			
DR	Pfam; PF00670; AdoHcyase_NAD; 1.			
DR	TIGRFAMs; TIGR00936; ancyl; 1.			
DR	PROSITE; PS00738; ADOHCYASE_1; 1.			
DR	PROSITE; PS00739; ADOHCYASE_2; UNKNOWN_1.			
KW	Hydrolase.			
SQ	SEQUENCE 500 AA; 55721 MW; 39A8F5E8D87A2DA CRC64;			
Query Match 80.1%; Score 1170; DB 2; Length 500;				
Best Local Similarity 92.1%; Pred. No. 9.3e-85;				
Matches 223; Conservative 10; Mismatches 7; Indels 2; Gaps 1				
Qy	41	QLOFA--DDMOEFTKPTPTKTGRSLRSISOSSTDSYSSAASYTSSDDEVSFRRQOTN	98	
Db	9	RIGPANDDKKEFSKPTKTGRSLRSISOSSTDSYSSAASYTSSDDEVSFRRQOTN	68	

QY	99	SKGSNFCVKNKIQKAEFRREIEIEAEQMSALISLRKKAQGEKPLAGAGIVCTHTTAOT	158
Db	69	SKGSSDFCVNKKQAEFRREIEIEAEQMSALISLRKKAQGEKPLAGAGIVCTHTTAOT	128
QY	159	AVLEETLCALGAQCRWSACNISTYSTONEVAALAEAGVAVPFAWKGSEDDFMWICDCVNM	218
Db	129	AVLEETLVALGAQCRMTACNISTYSTONEVAALAEAGSVFPAWKGSEDDFMWICDLVNM	188
QY	219	DGMQANMLDDGSGULTHWVYKKYPRVFKKINGIVEASTGVHRLYQLSKAGLTCVPMNV	278
Db	189	DGMQANMLDDGSGULTHWVYKKYPSVFVKRIVGIVEASTGVHRLYQLSKAGLTCVPMNV	248
QY	279	ND 280	
Db	249	ND 250	

RESULT 15

QARXQ1	TEITNG	PRELIMINARY;	PRT;	491 AA.	
AC	QARXQ1	TEITNG	PRELIMINARY;	PRT;	491 AA.
DT	19-JUL-2005,	integrated into UniProtKB/TrEMBL.			
DT	19-JUL-2005,	sequence version 1.			
DT	07-FEB-2006,	entry version 5.			
DE	Chromosome 11 SCAP14979,	5.			
GN	ORName=GSTENG00027329001;				
OS	Tetraodon nigroviridis (Green puffer);				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorphi; Acanthopterygii; Percormorpha; Tetraodontiformes;				
OC	Tetraodonidae; Tetraodontidae; Tetraodon.				
OX	NCBI_Taxid=99883;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RX	PubMed=15496914; DOI=10.1038/nature03025;				
RA	Jallion O., Aury J.-M., Brunet F., Petit J.-L., Searge-Thomann N.,				
RA	Maucel E., Bouneau L., Fischer C., Ozouf-Costes C., Bernot A.,				
RA	Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dessat C., Segreus B.,				
RA	Desliva C., Salomibat M., Levy M., Bondet N., Castellano S.,				
RA	Antoine C., Jabin C., Castelli V., Katinka M., Vacherie B.,				
RA	Blemond C., Skalli Z., Caticolico L., Poulain J., De Bernardis V.,				
RA	Cruaud C., Dupret S., Broctier P., Coutanceau J.-P., Gouzy J.,				
RA	Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,				
RA	Kellis M., Wolff J.-N., Guigo R., Zody M.C., Mesirov J.,				
RA	Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,				
RA	Landre V., Schachter V., Quetier F., Saurin W., Scarpelli C.,				
RA	Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.,				
RT	"Genome duplication in the teleost fish Tetraodon nigroviridis reveals				
RT	the early vertebrate proto-karyotype.";				
RL	Nature 431:946-957(2004).				
RN	[2]				
RP	NUCLEOTIDE SEQUENCE.				
RG	Genoscope; Whitehead Institute Centre for Genome Research;				
RL	Submitted (FEB-2004) to the EMBL/Genbank/DBJ databases.				
CC	-1- CAUTION: The sequence shown here is derived from an				
CC	EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is				
CC	preliminary data.				
CC	-1- CATALYTIC ACTIVITY: S-adenosyl-L-homocysteine + H(2)O = L-				
CC	homocysteine + adenosine.				
CC	-1- COFACTOR: NAD (By similarity).				
CC	-1- PATHWAY: Activated methyl cycle.				
CC	-1- SIMILARITY: Belongs to the adenosylhomocysteinase family.				
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms				
CC	Distributed under the Creative Commons Attribution-NoDerivs License				
CC	EMBL; CAAB01014979; CAG06831.1; -; Genomic DNA.				
DR	GO; GO:0004013; F:adenosylhomocysteinase activity; IEA.				
DR	GO; GO:0016787; F:hydrolyase activity; IEA.				
DR	GO; GO:0006730; P:one-carbon compound metabolism; IEA.				
DR	InterPro; IPR000043; Ad_hcy_hydrolyase.				
DR	PANTHER; PTHR11784; Ad_hcy_hydrolyase; 1.				

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:30:04 ; Search time 28 seconds
(without alignments)
875.306 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_280
Perfect score: 1461
Sequence: 1 MEMPDMPLPGVGEELKQAK.....RLVQLSKAGKLCVPMNVND 280

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /EMC_Celerra_SIDS3/ptodata/2/1aa/5_COMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/1aa/6_COMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/1aa/7_COMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/1aa/H_COMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/1aa/PCTUS_COMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/1aa/RE_COMB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/1aa/backfill1es1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1298	88.8	500	1 US-08-896-005-1	Sequence 1, Appl1
2	772	52.8	504	1 US-08-896-005-3	Sequence 3, Appl1
3	563	38.5	502	2 US-09-252-991A-23501	Sequence 23501, A
4	555	38.0	463	2 US-09-328-352-4600	Sequence 4600, Ap
5	513	35.1	515	2 US-09-248-796A-18264	Sequence 18264, A
6	509	34.8	432	1 US-08-896-005-4	Sequence 5, Appl1
7	504	34.5	432	1 US-08-896-005-4	Sequence 4, Appl1
8	504	34.5	432	2 US-09-347-878-1	Sequence 1, Appl1
9	504	34.5	432	2 US-09-546-013-3	Sequence 3, Appl1
10	503	34.4	447	2 US-09-849-016-10359	Sequence 10359, A
11	456.5	31.2	498	2 US-09-919-854-2	Sequence 2, Appl1
12	416	28.5	486	2 US-08-930-894-2	Sequence 2, Appl1
13	392.5	26.9	476	2 US-09-759-990A-7	Sequence 7, Appl1
14	390	26.7	476	2 US-09-902-540-10728	Sequence 10728, A
15	312	21.4	99	2 US-08-930-894-8	Sequence 8, Appl1
16	312	21.4	139	2 US-08-930-894-6	Sequence 6, Appl1
17	211	14.4	97	1 US-08-204-740-7	Sequence 7, Appl1
18	211	14.4	97	2 US-09-081-167A-7	Sequence 7, Appl1
19	211	14.4	97	2 US-09-081-167A-7	Sequence 7, Appl1
20	211	14.4	97	2 US-09-416-833-7	Sequence 7, Appl1
21	211	14.4	97	5 PCT-US95-02521-7	Sequence 7, Appl1
22	205.5	14.1	138	2 US-08-930-894-5	Sequence 5, Appl1
23	204	14.0	81	2 US-09-513-999C-5599	Sequence 5999, Ap
24	203.5	13.9	140	2 US-08-930-894-4	Sequence 4, Appl1
25	196.5	13.4	95	1 US-08-204-740-9	Sequence 9, Appl1
26	196.5	13.4	95	2 US-09-081-167A-9	Sequence 9, Appl1

27	196.5	13.4	95	2 US-09-081-395-9	Sequence 9, Appl1
28	196.5	13.4	95	2 US-09-416-833-9	Sequence 9, Appl1
29	196.5	13.4	95	5 PCT-US95-02521-9	Sequence 7, Appl1
30	182	12.5	139	2 US-08-930-894-7	Sequence 7, Appl1
31	140	9.6	387	2 US-09-489-039A-8393	Sequence 8393, Ap
32	95	6.5	324	1 US-07-667-276A-4	Sequence 4, Appl1
33	88	6.0	414	1 US-09-248-796A-17156	Sequence 17156, A
34	88	6.0	466	1 US-08-194-338-11	Sequence 11, Appl1
35	88	6.0	542	2 US-09-538-092-289	Sequence 289, Ap
36	86.5	5.9	703	2 US-08-910-925-4	Sequence 4, Appl1
37	86	5.9	792	2 US-09-248-796A-18842	Sequence 18842, A
38	85.5	5.9	290	1 US-08-903-801-1	Sequence 1, Appl1
39	85.5	5.9	290	2 US-09-295-055-1	Sequence 1, Appl1
40	85.5	5.9	699	2 US-10-104-047-2814	Sequence 2814, Ap
41	85.5	5.9	800	2 US-09-252-991A-20437	Sequence 20437, A
42	85.5	5.9	1031	2 US-09-585-1738-40	Sequence 40, Appl1
43	84.5	5.8	130	1 US-08-630-822A-90	Sequence 90, Appl1
44	84.5	5.8	130	1 US-09-005-069-90	Sequence 90, Appl1
45	84.5	5.8	130	2 US-09-171-156A-39	Sequence 39, Appl1

ALIGNMENTS

RESULT 1
US-08-896-005-1
Sequence 1, Application US/08896005
Patent No. 5854023
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Ial, Preeti
APPLICANT: Shah, Puri
NUMBER OF INVENTIONS: 5
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,005
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0337 US
TELEPHONE/COMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 500 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
CLONE: 1519044
US-08-896-005-1
Query Match 88.8%; Score 1298; DB 1; Length 500;
Best Local Similarity 99.6%; Pred. No. 7.4e-140;

SEQ ID NO 4600
LENGTH: 463
TYPE: PR
ORGANISM: Acinetobacter baumannii
US-09-328-352-4600

Query Match 38.0%; Score 555; DB 2; Length 463;
Best Local Similarity 57.2%; Pred. No. 1,3e-54;
Matches 103; Conservative 38; Mismatches 37; Indels 2; Gaps 1;

QY 103 SNFCVKNIKOAEFRREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTAQTAVLI 162
DB 12 TDYKVDADISLADYGRKEIKIAEAMPAALIGRKRYASKPLAGKICGCHMTITQTAVLI 71
QY 163 ETLALGAQCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWWCIDRCVNDG-- 220
DB 72 ETLVEIGAEVWMTSCNIFSTODHAAAIAARGIVFAMKETEVEEYWCIEQOINVNGP 131
QY 221 WQANMLDDGGDLTHWYKRYPNVFKIRGIVESVTVGVRHLVQLSKAGLCVPMANVND 280
DB 132 WQANMLDDGGDLTHWYKRYPNVFKIRGIVESVTVGVRHLVQLSKAGLCVPMANVND 191

RESULT 5
US-09-248-796A-18264
Sequence 18264, Application US/09248796A
Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248.796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18264

LENGTH: 515
TYPE: PR
ORGANISM: Candida albicans
US-09-248-796A-18264

Query Match 35.1%; Score 513; DB 2; Length 515;
Best Local Similarity 53.0%; Pred. No. 1e-49;
Matches 98; Conservative 38; Mismatches 47; Indels 2; Gaps 1;

QY 98 NKGSSNFCVKNIKOAEFRREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTAQTAVLI 157
DB 67 SSAPANNYVADISLAFGRKDIETSENEPGLMYIRKKGPSQPLKGAIRIACCLHMTITQ 126
QY 158 TAVLIETTLALGAQCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWWCIDRCVNDG--C 215
DB 127 TAVLIETTLALGAQCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWWCIDRCVNDG--C 215
QY 216 VNMDSQANMLDDGGDLTHWYKRYPNVFKIRGIVESVTVGVRHLVQLSKAGLCVPMANVND 275
DB 187 AFKDGKMLLDDGGDLTHWYKRYPNVFKIRGIVESVTVGVRHLVQLSKAGLCVPMANVND 246
QY 276 NMVND 280
DB 247 INVND 251

RESULT 6
US-08-896-005-5
Sequence 5, Application US/08896005
Patent No. 5854023
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.

APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/896,005
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0337 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 904132
US-08-896-005-5.

Query Match 34.8%; Score 509; DB 1; Length 432;
Best Local Similarity 53.4%; Pred. No. 2,2e-49;
Matches 93; Conservative 36; Mismatches 45; Indels 0; Gaps 0;

QY 107 VKNIKOAEFRREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHTAQTAVLIETLC 166
DB 9 VADIGLAAGRALDIAENEMPGLMRMREYSASKPLKGAIRIACCLHMTITVETAVLIETLV 68
QY 167 ALGAQCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWWCIDRCVNDGQANMI 226
DB 69 ALGAQCRWSACNIYSTONEVAALAEAGVAFAMKGESEDDFWWCIDRCVNDGQANMI 128
QY 227 LDDGGDLTHWYKRYPNVFKIRGIVESVTVGVRHLVQLSKAGLCVPMANVND 280
DB 129 LDDGGDLTHWYKRYPNVFKIRGIVESVTVGVRHLVQLSKAGLCVPMANVND 182

RESULT 7
US-08-896-005-4
Sequence 4, Application US/08896005
Patent No. 5854023
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA

```

:
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/896,005
: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0337 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 432 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: GenBank
: CLONE: 178277
:
: US-08-896-005-4
:

```

Query Match	34.5%	Score 504;	DB 1;	Length 432;
Best Local Similarity	52.9%;	Pred. No. 8.4e-49;		
Matches 92;	Conservative 36;	Mismatches 46;	Indels 0;	Gaps 0

QY VKQIKOAEFRRIEIEAEDMSALISLRRAQGEPLAGAKIVGTHITTAQTAVALIELC 166
 10 VAIIGLAAWRKALDIAENMPEGLMKRRERYASRXLPGARLAGCLHMTVETAVILIELV 68
 Db 9
 QY ALGAGCRMSACNIYSTONEVAAALAEAGAAVEAMKGESEDDFWMCIDRCVNNDGQANMI 226
 167
 69 TLGAEVQWSSCNFTSTONHAAAAIAKAGIPVYAMGEDEDELTNCIETOTLPKQGPLNMI 128
 Db
 QY LDDGGDLTHWVYKKYPNVFEKIRIGIYEESVTVHRLLYQHSKAGKLCVAMNVND 280
 227
 Db LDDGGDLTHIRIKYVYQPLPGIRGISSEETTTGVNHLKMMANGILKVAIVNND 162

```

RESULT 8
US-09-347-878-1
; Sequence 1, Application US/09347878C
; Patent No. 6376210
; GENERAL INFORMATION:
; APPLICANT: Yuan, Chong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
; FILE REFERENCE: 25885-1651
; CURRENT APPLICATION NUMBER: US/09/347, 878C
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ. ID NOS: 75
; SOFTWARE: PatentIn Ver. 2.0

```

LENGTH: 432

```

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```

OTHER INFORMATION: Human S-adenosylhomocysteine hydrolase protein

PUBLICATION INFORMATION:

! DATABASE ACCESSION NUMBER: M61831/Genbank
US-09-347-878-1

Query Match	34.5%	Score 504;	DB 2;	Length 432
Best Local Similarity	52.9%	Pred. No. 8.4e-49;		

Matches	92;	Conservative	36;	Mismatches	46;	Indels	0;	Gaps	0;
---------	-----	--------------	-----	------------	-----	--------	----	------	----

Oy	167	ALGAOCMSACNIYSTONEVAAALAEAGVAVFAKGESEDDFWMCIDRCVMNDGQANMI	226
Dd	69	TLAGAEVOMSSCNIFSTONHAAAAIAXAGCIPYANKGETDEBYLMCIBETLYFXDGPLNMI	128
Oy	227	LDDGGDLTHWWYYKKYPNVFCKIRIGIVESVTVGHRLYQLSKAGKLCPVPMNVND	280
Dd	129	LDDGGDLTNLHTKYPPQLPGIRISSETTTGVGHVNLKXMANGLTKVPAINVD	182

RESULT 9
US-09-546-013-3
Sequence 3, Application US/09546013

```

1  APPLICANT: Yuan, Chong-Shen
2  TITLE OF INVENTION: METHODS FOR ASSAYING S-ADENOSYLMETHIONINE-DEPENDENT Methyltransferase
3  FILE REFERENCE: 10937-1652
4  CURRENT APPLICATION NUMBER: US/09/546,013
5  CURRENT FILING DATE: 2000-04-10
6  EARLIER APPLICATION NUMBER: 09/347,878
7  EARLIER FILING DATE: 1999-07-06
8  EARLIER APPLICATION NUMBER: 09/457,205
9  EARLIER FILING DATE: 1999-12-06
10 NUMBER OF SEQ ID NOS: 94
11 SOFTWARE: PatentIn Ver. 2.0
12 SEQ ID NO 3
13

```

```

: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: Human S-adenosylhomocysteine hydrolase protein
: OTHER INFORMATION: sequence
: PUBLICATION INFORMATION:
: DATABASE ACCESSION NUMBER: M61311/genbank
: JS-09-546-013-3

```

Query Match	34.5%	Score 504;	DB 2;	Length 432;
-------------	-------	------------	-------	-------------

Best Local Similarity 52.9%; Pred. No. 8.4e-49;
Matches 92; Conservative 36; Mismatches 46; Indels 0; Gaps 0.

```

Qy      107 VKRIQAFFGRREIEIAEDMSALISLRKAQGEPLAGAKIVGCHITAOAVLIELTC 166
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      9  VAIIGLAWGRKALDIAENENMPGLRMREYRSASPLKGARIAGCLHMTVEAVLIELTV 68

```

```
OY      167 ALGAQCRPSACNITYSTONEVAALLAEAGAVFPAWKGESEDDFWWCIDRCVNNIDGMQNMI    226  
       .|||:|||:|||::|||:|||::|||::::|::|:  
DB     69 TLGAEVGSSCNIFSTGNHAAAALAKAGIPVYAWKGETDEEYLWTCIEQTLYFKDGPLMI   128
```

QY 227 LDDGDDLTHWVYKKKPNVFKIRGIVESTGVHRLYQLSLAGKLCVAPANNVD 280
 |||||:::||||:|||||:::||||:||||
 Db 129 LDDGDDLTHLHTRKPOLLPGRIGISEETTTGVHNLTKMMANGILKVPAINVD 182

RESULT 10
US-09-949-016-10359

Sequence 10359, Application US/09949016
Patent No. 6812339

; GENERAL INFORMATION:

APPLICANT: VENIER, J. Craig et al

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE METHODS OF DETECTING

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USE THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/94
CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: 60/241,133
FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-20
PUB. NO.: 60/337 768

FRISK AFFLICTION NUMBER: 88/237, 100

US-09-759-990A-7
; Sequence 7, Application US/09759990A
; Patent No. 671373
; GENERAL INFORMATION:
; APPLICANT: Anticancer, Inc.
; APPLICANT: Xu, Mingxu
; APPLICANT: Han, Qinghong
; TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH
; TITLE OF INVENTION: SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE
; FILE REFERENCE: 31276-20026.00
; CURRENT APPLICATION NUMBER: US/09/759,990A
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/176,444
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Faeseq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-990A-7
Query Match 26.9%; Score 392.5; DB 2; Length 486;
Best Local Similarity 39.4%; Pred. No. 6.4e-36;
Matches 87; Conservative 30; Mismatches 57; Indels 47; Gaps 4;
QY 107 VKNIKQAEFRREIEIAEQMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLIETLC 166
DB 15 IADINHLVLRKELTLAEKEMVLRERYSASKPLKGVRISSLHMTVQTAVLIETLT 74
QY 167 ALGAQCWMSKCNISTONEVAALAA-----EAGVAFAMGSEDDPFMCIDRCVN 217
DB 75 ALGADYRMASCNIFSTODTAAALVVGPTGTPKPKAGIPVAMGKFTLPYEWENTYFALT 134
QY 218 M-DGMQANMLIDGGDLTHWVYKY-----PNVFKK--- 247
DB 135 WPGGQGGQGVVDDGGDTLLISKFEFETAGVPEPEADNLEKRCVLAFLKQVFNQDKN 194
QY 248 -----IRGIVEESYGVHRLYOLSKAGLCVPMANNVD 280
DB 195 HMHTVAAGMNGVSEETTTGVHRLYOLSKAGLCVPMANNVD 235
RESULT 14
US-09-902-540-10728
; Sequence 10728, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10728
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10728
Query Match 26.7%; Score 390; DB 2; Length 476;
Best Local Similarity 39.6%; Pred. No. 1.2e-35;
Matches 86; Conservative 35; Mismatches 56; Indels 40; Gaps 3;
QY 104 NFGVNIKQAEFRREIEIAEQMSALISLRKQAGEKPLAGAKIVGCTHTTAQTAVLI 163
DB 11 DVAIADLSLADWGRKEIRIAESEMPALMAIREYAKTQPIKGAIVTGSLSHMTIQTAVLVE 70

QY 164 TLGALGQCWMSKCNISTONEVAALAAEAGVAFAMKGESEDDPFMCIDRCVNM----- 218
DB 71 TLQALGAEVFMASCNIFSTODHAAALVQAGTVPFAHKBSLKEYDFTIRIDFGPAGS 130
QY 219 DGMQANMLIDGGDLTHWVY--KK-----YPN 243
DB 131 DHEGPNMLIDGGDATTLLHGLKRAEKDASVLANPOSEBERELYYAIKAKLAEDATYTR 190
QY 244 VFKIRGIVEESYGVHRLYOLSKAGLCVPMANNVD 280
DB 191 KSAKILIGVEETTTGVHRLQEMSAKGTLLFRALNVND 227
RESULT 15
US-08-930-894-8
; Sequence 8, Application US/08930894
; Patent No. 6037524
; GENERAL INFORMATION:
; APPLICANT: GREENLAND, Andrew James
; APPLICANT: DRAVER, John
; APPLICANT: SKIPSEY, Marc
; APPLICANT: WARNER, Simon
; TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOTER
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Madison & Sutro
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,894
; FILING DATE: 09-OCT-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB96/00882
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507381.3
; FILING DATE: 10-APR-1995
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 99 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: WHEAT SHH PROTEIN (2)
US-08-930-894-8
Query Match 21.4%; Score 312; DB 2; Length 99;
Best Local Similarity 57.1%; Pred. No. 9.1e-28;
Matches 56; Conservative 20; Mismatches 20; Indels 2; Gaps 1;
QY 185 EVAALAEAGVAFAMKGESEDDPFMCIDRCVNMDS--WOANNMLIDGGDLTHWVYKYR 242
DB 1 QAAALAAAGTVPFAKGEETEEYEWCTIOTIKDGKPMDDANNVLDGGDLTILHKKYP 60
QY 243 NVFKIRGIVEESYGVHRLYOLSKAGLCVPMANNVD 280
DB 61 QMURIRHIGTEETTTGVHRLMLKAGTLKVPALNVNN 98
Search completed: September 6, 2006, 19:32:24
Job time : 29 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:51:30 ; Search time 93.1304 Seconds
(without alignments)
1392.672 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_280
Perfect score: 1461
Sequence: 1 MSPDPAMPPLPGVGEELKQAK.....RLYQLSKAGKLCVPMANVND 280

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1461	100.0	530	US-10-876-285-2	Sequence 2, Appli
2	1461	100.0	530	US-10-876-285-4	Sequence 4, Appli
3	1461	100.0	530	US-10-876-285-6	Sequence 6, Appli
4	1461	100.0	530	US-10-876-285-8	Sequence 8, Appli
5	1461	100.0	530	US-10-683-610-1	Sequence 1, Appli
6	1461	100.0	614	US-09-782-051-2	Sequence 2, Appli
7	1461	100.0	614	US-11-110-748-2	Sequence 2, Appli
8	1155.5	79.1	455	US-10-450-763-42388	Sequence 42388, A
9	1155.5	79.1	619	US-10-756-149-5569	Sequence 5569, Ap
10	1140	78.0	564	US-10-467-903-1	Sequence 1, Appli
11	847	58.0	521	US-11-097-143-2781	Sequence 2781, Ap
12	772	55.8	504	US-11-097-143-41922	Sequence 41922, A
13	746	51.1	239	US-09-925-300-1379	Sequence 1379, Ap
14	610.5	41.8	257	US-10-424-599-212758	Sequence 212758
15	549	37.6	466	US-10-369-493-13881	Sequence 13881, A
16	527	36.1	426	US-10-369-493-10135	Sequence 10135, A
17	526	36.0	447	US-10-369-493-3683	Sequence 3683, Ap
18	520	35.6	433	US-10-369-493-2425	Sequence 2425, Ap
19	520	35.6	433	US-10-369-493-2430	Sequence 2430, Ap
20	516.5	35.4	432	US-11-097-143-39477	Sequence 39477, A
21	511	35.0	449	US-10-369-493-1740	Sequence 1740, Ap
22	505	34.6	433	US-10-433-802-4	Sequence 4, Appli
23	504.5	34.5	457	US-09-925-301-1059	Sequence 1059, Ap
24	504	34.5	432	US-10-836-953-1	Sequence 1, Appli
25	502.5	33.4	437	US-10-369-493-5097	Sequence 5097, Ap
26	487	33.3	428	US-10-369-493-10445	Sequence 10445, A
27	482.5	33.0	168	US-10-425-115-244651	Sequence 244651, A

28	480.5	32.9	499	6	US-11-079-463-7902	Sequence 7902, Ap
29	474.5	32.5	469	4	US-10-314-657-71	Sequence 71, Appl
30	474.5	32.5	469	5	US-10-473-193-71	Sequence 71, Appl
31	463.5	31.7	485	4	US-10-156-761-12587	Sequence 12587, A
32	459.5	31.5	476	4	US-10-369-493-8266	Sequence 8266, Ap
33	457	31.3	485	4	US-10-767-701-47244	Sequence 47244, A
34	456.5	31.2	432	3	US-09-746-660A-102	Sequence 102, App
35	456.5	31.2	432	3	US-11-055-822-224	Sequence 224, App
36	456.5	31.2	432	6	US-11-239-674-102	Sequence 102, App
37	456.5	31.2	474	3	US-09-738-626-4336	Sequence 4336, Ap
38	456.5	31.2	478	3	US-09-746-660A-98	Sequence 98, Appl
39	456.5	31.2	478	6	US-11-055-822-220	Sequence 220, App
40	456.5	31.2	478	6	US-11-239-674-98	Sequence 98, Appl
41	456.5	31.2	498	3	US-09-919-854-2	Sequence 2, Appli
42	455	31.1	465	4	US-10-369-493-17934	Sequence 17934, A
43	454.5	31.1	516	4	US-10-369-493-13111	Sequence 13111, A
44	453	31.0	463	4	US-10-369-493-20829	Sequence 20829, A
45	453	31.0	466	4	US-10-369-493-12110	Sequence 12110, A

ALIGNMENTS

RESULT 1
US-10-876-285-2
Sequence 2, Application US/10876285
Publication No. US20050044582A1
GENERAL INFORMATION:
APPLICANT: Kato, Masato
APPLICANT: Angel, Nicola
APPLICANT: Cooper, Benjamin Jay
APPLICANT: Hart, Derek
TITLE OF INVENTION: Novel Polynucleotides and uses therefor
FILE REFERENCE: 10338-18US
CURRENT APPLICATION NUMBER: US/10/876,285
CURRENT FILING DATE: 2004-06-24
PRIOR APPLICATION NUMBER: PR9741/01
PRIOR FILING DATE: 2001-12-24
PRIOR APPLICATION NUMBER: PCT/AU02/01761
PRIOR FILING DATE: 2002-12-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 530
TYPE: PRT
ORGANISM: human
US-10-876-285-2

Query Match	100.0%	Score 1461;	DB 5;	Length 530;
Best Local Similarity	100.0%	Pred. No. 5.4e-132;		
Matches 280;	Conservative	0;	Mismatches 0;	Indels 0;
			Gaps 0;	
QY	1	MSPDPAMPPLPGVGEELKQAKIEDAKESFMAITVYKAKKQIOFADMOEFTKPTKGR	60	
DB	1	MSPDPAMPPLPGVGEELKQAKIEDAKESFMAITVYKAKKQIOFADMOEFTKPTKGR	60	
QY	61	RLSLRSISQSTSDYSYSAASTTSSDDEVSPEKQOITNSKSSNFCVKKIKOAEFGREI	120	
DB	61	RLSLRSISQSTSDYSYSAASTTSSDDEVSPEKQOITNSKSSNFCVKKIKOAEFGREI	120	
QY	121	ELAEQDMALSLRRPAGGKPLAGAKIVGCTHTTAOTRAVLIELTCAAGOCRSACIN	180	
DB	121	ELAEQDMALSLRRPAGGKPLAGAKIVGCTHTTAOTRAVLIELTCAAGOCRSACIN	180	
QY	181	STONEVAALAEAGVAFVAMKGESEDDFMWCIDRCVNNDMGQANNITLDDGDLTHVYKK	240	
DB	181	STONEVAALAEAGVAFVAMKGESEDDFMWCIDRCVNNDMGQANNITLDDGDLTHVYKK	240	
QY	241	YPNVFKTKIRGIVBSVTGVHRLYQLSKAGKLCVPMANVND 280		
DB	241	YPNVFKTKIRGIVBSVTGVHRLYQLSKAGKLCVPMANVND 280		

```
RESULT 2
US-10-876-285-4
; Sequence 4, Application US/10876285
; Publication No. US20050044582A1
GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Human
US-10-876-285-4

Query Match      100.0%; Score 1461; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 5,4e-132;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPJPGVGEELKQAKETIEDAEKYSFMAVTYKAPKKQIOFADDMOEFKPKTKGR 60
DB 1 MSMPDAMPJPGVGEELKQAKETIEDAEKYSFMAVTYKAPKKQIOFADDMOEFKPKTKGR 60
QY 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVKNIKQAEFGRRREI 120
DB 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVKNIKQAEFGRRREI 120
QY 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRMSACNIIY 180
DB 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRMSACNIIY 180
QY 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMDSQWQANMILDDGGDLTHWVYKK 240
DB 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMDSQWQANMILDDGGDLTHWVYKK 240
QY 241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANNVND 280
DB 241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANNVND 280

RESULT 3
US-10-876-285-6
; Sequence 6, Application US/10876285
; Publication No. US20050044582A1
GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
```

```
US-10-876-285-6

Query Match      100.0%; Score 1461; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 5,4e-132;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPJPGVGEELKQAKETIEDAEKYSFMAVTYKAPKKQIOFADDMOEFKPKTKGR 60
DB 1 MSMPDAMPJPGVGEELKQAKETIEDAEKYSFMAVTYKAPKKQIOFADDMOEFKPKTKGR 60
QY 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVKNIKQAEFGRRREI 120
DB 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVKNIKQAEFGRRREI 120
QY 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRMSACNIIY 180
DB 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRMSACNIIY 180
QY 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMDSQWQANMILDDGGDLTHWVYKK 240
DB 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMDSQWQANMILDDGGDLTHWVYKK 240
QY 241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANNVND 280
DB 241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANNVND 280

RESULT 4
US-10-876-285-8
; Sequence 8, Application US/10876285
; Publication No. US20050044582A1
GENERAL INFORMATION:
; APPLICANT: Kato, Masato
; APPLICANT: Angel, Nicola Zoe
; APPLICANT: Cooper, Benjamin Jay
; APPLICANT: Hart, Derek Nigel John
; TITLE OF INVENTION: Novel Polynucleotides and uses therefor
; FILE REFERENCE: 10338-18US
; CURRENT APPLICATION NUMBER: US/10/876,285
; CURRENT FILING DATE: 2004-06-24
; PRIOR APPLICATION NUMBER: PR9741/01
; PRIOR FILING DATE: 2001-12-24
; PRIOR APPLICATION NUMBER: PCT/AU02/01761
; PRIOR FILING DATE: 2002-12-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mouse
US-10-876-285-8

Query Match      100.0%; Score 1461; DB 5; Length 530;
Best Local Similarity 100.0%; Pred. No. 5,4e-132;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSMPDAMPJPGVGEELKQAKETIEDAEKYSFMAVTYKAPKKQIOFADDMOEFKPKTKGR 60
DB 1 MSMPDAMPJPGVGEELKQAKETIEDAEKYSFMAVTYKAPKKQIOFADDMOEFKPKTKGR 60
QY 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVKNIKQAEFGRRREI 120
DB 61 RLSRSISQSSSTDSYSSAASYTDSDEVSPPREKQOTNSKGSNFCVKNIKQAEFGRRREI 120
QY 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRMSACNIIY 180
DB 121 EIAEQDMSALISLRKRAQGEKPLAGAKIVGCTHTTAQTAVLIETLCAAGQCRMSACNIIY 180
QY 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMDSQWQANMILDDGGDLTHWVYKK 240
DB 181 STONEVAAAALAEAGVAVFAMKGESEDDFWWCIDRCVNMDSQWQANMILDDGGDLTHWVYKK 240
QY 241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANNVND 280
DB 241 YPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPANNVND 280
```

Db 241 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 280

```

RESULT 5
US-10-683-610-1
; Sequence 1, Application US/10683610
; Publication No. US20050181450A1
; GENERAL INFORMATION:
; APPLICANT: RIKEN
; TITLE OF INVENTION: A novel inositol 1,4,5-trisphosphate (IP3) receptor binding prote
; TITLE OF INVENTION: IP3
; TITLE OF INVENTION: indicator
; FILE REFERENCE: PH-1852
; CURRENT APPLICATION NUMBER: US/10/683,610
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: JP 2002-299429
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 530
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-683-610-1

```

Query Match 100.0%; Score 1461; DB 5; Length 530;
 Best Local Similarity 100.0%; Pred. No. 5,4e-132;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 60
DB 1 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 60
QY 61 RLSRSISQSSSTDSYSSAASYTDSDDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
DB 61 RLSRSISQSSSTDSYSSAASYTDSDDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
QY 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHITTAQAVLIETTCALGAOCRWSACNII 180
DB 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHITTAQAVLIETTCALGAOCRWSACNII 180
QY 181 STONEVAAAALAEAGAVAFAMKGESEDDFWWCIDRCVNMGMQANNILDDGGDLTHWVYK 240
DB 181 STONEVAAAALAEAGAVAFAMKGESEDDFWWCIDRCVNMGMQANNILDDGGDLTHWVYK 240
QY 241 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 280
DB 241 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 280

```

```

RESULT 6
US-09-782-051-2
; Sequence 2, Application US/09782051
; Patent No. US20020035078A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
; TITLE OF INVENTION: (AHCV) type activity
; FILE REFERENCE: 24305 MRB
; CURRENT APPLICATION NUMBER: US/09/782,051
; CURRENT FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: PCT/NZ97/00133
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: NZ 299507
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-782-051-2

```

Query Match 100.0%; Score 1461; DB 3; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6,7e-132;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 60
DB 85 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 144
QY 61 RLSRSISQSSSTDSYSSAASYTDSDDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
DB 145 RLSRSISQSSSTDSYSSAASYTDSDDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 204
QY 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHITTAQAVLIETTCALGAOCRWSACNII 180
DB 205 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHITTAQAVLIETTCALGAOCRWSACNII 264
QY 181 STONEVAAAALAEAGAVAFAMKGESEDDFWWCIDRCVNMGMQANNILDDGGDLTHWVYK 240
DB 265 STONEVAAAALAEAGAVAFAMKGESEDDFWWCIDRCVNMGMQANNILDDGGDLTHWVYK 324
QY 241 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 280
DB 325 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 364

```

Query Match 100.0%; Score 1461; DB 6; Length 614;
 Best Local Similarity 100.0%; Pred. No. 6,7e-132;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

RESULT 7
US-11-110-748-2
; Sequence 2, Application US/11110748
; Publication No. US20050282765A1
; GENERAL INFORMATION:
; APPLICANT: Hart, Derek N J
; TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
; TITLE OF INVENTION: (AHCV) type activity
; FILE REFERENCE: 24305 MRB
; CURRENT APPLICATION NUMBER: US/11/110,748
; CURRENT FILING DATE: 2005-04-21
; PRIOR APPLICATION NUMBER: PCT/NZ97/00133
; PRIOR FILING DATE: 1997-10-06
; PRIOR APPLICATION NUMBER: NZ 299507
; PRIOR FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-110-748-2

```

```

QY 1 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 60
DB 85 MSMPAMPPLPGVGEELKQAKIEDAEKYSFMAVTYKAPKKQIQFADDMQEFTRPKTKGR 144
QY 61 RLSRSISQSSSTDSYSSAASYTDSDDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 120
DB 145 RLSRSISQSSSTDSYSSAASYTDSDDDEVSPPREKQOTNSKSSNFCVKNIKQAEFGRRRI 204
QY 121 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHITTAQAVLIETTCALGAOCRWSACNII 180
DB 205 EIAEDMSALISLRKRAQGEKPLAGAKIVGCTHITTAQAVLIETTCALGAOCRWSACNII 264
QY 181 STONEVAAAALAEAGAVAFAMKGESEDDFWWCIDRCVNMGMQANNILDDGGDLTHWVYK 240
DB 265 STONEVAAAALAEAGAVAFAMKGESEDDFWWCIDRCVNMGMQANNILDDGGDLTHWVYK 324
QY 241 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 280
DB 325 YNNVFKIRGIYESVTGVHRLYQLSKAGKLCVPANNVND 364

```

```

RESULT 8
US-10-450-763-42388
; Sequence 42388, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790Cf3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 42388
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (356)..(388)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase proteins domain
; OTHER INFORMATION: identified by eMARTIX, accession number BL00738F, p-value=7.261e-
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (186)..(447)
; OTHER INFORMATION: S-adenosyl-L-homocysteine hydrolase domain identified by
; OTHER INFORMATION: Pram, accession name AdoHcyase, E-value=6.2e-171, Pram score of
US-10-450-763-42388

Query Match 79.1%; Score 1155.5; DB 5; Length 455;
Best Local Similarity 75.3%; Pred. No. 1,4e-102;
Matches 226; Conservative 24; Mismatches 23; Indels 27; Gaps 3;

QY 8 PLPGVGE-----ELKQAKEIEDAEKY-----SFMATVYAKP--K 40
Db 61 PVPGGSGPALALSPAGKVPQASAMKRSDPHQHQRHRRDGEALVSPDGTVEAPRTVK 120

QY 41 QIQPDDMOETTKPPTKTGRSLRSISQSSSTDYSLSAAYTDSDDDEVSPREKQOTNSK 100
Db 121 KIQPDDQKQEFNKRPKTIGRSLRSISQSSSTDYSLSAAYTDSDDDETSPDKQKXNSK 180

QY 101 GSSNFCVNIKQAEGRREIEIABEDMSALISLRKQAGEKPLAGAKIVGCTHITAOTAV 160
Db 181 GSSDFCVNIKQAEGRREIEIABEDMPALMLRKQAGEKPLAGAKIVGCTHITAOTAV 240

QY 161 LIETLCAIGACQCRMSACNIYSTONEVAALAEVAVFAWKGESDDFWKCIDRCVNMDG 220
Db 241 LMETLGAIGACQCRMAACNIYSTLINEVAALAESGEPVFAWKGESDDFWKCIDRCVNEG 300

QY 221 WOANMLIDGGDLTHWVYKKYPNVFKKIRGIVEESVTVHRLYOLSKAGKLCVPAMVND 280
Db 301 WQPNMLIDGGDLTHWYKKYPNMKFKKIRGIVEESVTVHRLYOLSKAGKLCVPAMVND 360

RESULT 9
US-10-756-149-5569
; Sequence 5569, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natsasha
; APPLICANT: Zlocnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF DIAGNOSIS OF METASTATIC CANCER, COMPOSITIONS ANT
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149

```

```

CURRENT FILING DATE: 2004-01-12
NUMBER OF SEQ ID NOS: 5818
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5569
LENGTH: 619
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-756-149--5569

Query Match          79.1%; Score 1155.5; DB 5; Length 619;
Best Local Similarity 75.3%; Pred. No. 2.2e-102;
Matches 226; Conservative 24; Mismatches 23; Indels 27; Gaps 3;

QY      PLPGVGE-----ELKQAKEIEDAEKY-----SFMAITVKAPK--K 40
Dg      PVCPGGSPAAALSSPAAGKVQAASAMRSDPHHQHRHDDGEGALVPDGTVTEAIPRVK 129
QY      QIQPADDMOEFETKPTKTGRSRISRSISQSSTDSYSAASYTDSDEVSPEKKOOTNSK 100
Db      KIQPADDKQEENRKPKTKIGRSSLSRSISQSSTDSYSASAATDSDBDETSPRDQQKN SK 189
QY      GGSNFCVNKIQAQFGRREIEIAEODMSALISTKRKAQGEXPLGAKIVGTHTIATAQTAV 160
Db      GSSDFCFKIKQAQFGGREIEIAEQEMPALMLFKRAQGXEPPLAGAKIVGTHTIATQAV 249
QY      LIETLCALGAOCNRSA CNISTONEVAALLAEAVANFAWKGESEEDPFMCIDBCVYNND 220
Db      LMETLGLALGAOCRRMACNIYSTLENEVAALAESGFVFAMWGESBEDPFMCIDECVAVEG 309
QY      WQNMIIIDDDGDLDHWYYKKYPNVFFKIRGIIVESVTGVHLRYOLSKRAGKLCTVPMANNVD 280
Db      WQPNMIIIDDDGDLDHWLYKKYPIPVNFKKIKGIIVESVTGVHLRYOLSKRAGKLCTVPMANNVD 369

RESULT 10
US-10-467-903-1
Sequence 1, Application US/10467903
Publication No. US20040265807A1
GENERAL INFORMATION:
APPLICANT: INCYTE CORPORATION
APPLICANT: SANJANAVALA, Madhusudan M.
APPLICANT: LU, Yan
APPLICANT: LEU, Ernestine A.
APPLICANT: HARALYA, April J.A.
APPLICANT: WARREN, Bridget A.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: TANG, Y. Tom
APPLICANT: YUE, Henry
APPLICANT: YAO, Monique G.
APPLICANT: LEE, Sally
APPLICANT: THORNTON, Michael B.
APPLICANT: CHAWLA, Narender K.
APPLICANT: XU, Yuming
APPLICANT: TRAN, Uyen K.
APPLICANT: TAL, Preeti G.
APPLICANT: LU, Dyung Alina M.
APPLICANT: SWARNAKAR, Anita
APPLICANT: KING, Huijun Z.
APPLICANT: JONES, Karen A.
TITLE OF INVENTION: ENZYMES
FILE REFERENCE: PI-0360 USN
CURRENT APPLICATION NUMBER: US/10/467,903
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: PCT/US02/03814
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/266,113
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/269,215
PRIOR FILING DATE: 2001-02-15
PRIOR APPLICATION NUMBER: US 60/272,271
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US 60/274,091
PRIOR FILING DATE: 2001-03-07

```

123 AEQDM\$ALISLRKRAQGEKPLAGAKI VGC'IH1IAQIAVLEILCALGAQCRWSACN1Y\$1 182

123 AEQDMSALISLRKRAQGEKPLAGAKIVGCIHIIAQIVALLLEILCALGAQCRWSACNIIYSI 182

```

Db      86 AEESEPMITLRRKAKDEKPKGNIVGCTHVNQSAVLLETLVQLATVYRMAACNTYST 145
QY      183 QNEVVAALAEAGVAVFAMKGESEDDFWMCIDRCVNMGMQMANILLDGGDLTHVVKYP 242
Db      146 QNVAALLAEIGITFAMRGTEEFPMWCDRALYSQGMONLLDDGGDATHLMKKYP 205
QY      243 NVEKIRGIVEESTVGVHRLYQLSKAGLCVPMANVD 280
Db      206 DYFKAIRGIVESVGVHRLYMLSKGRLTVPAINVND 243

```

RESULT 13

```

US-09-925-300-1379
; Sequence 1379, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruden,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/05388
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1379
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (229)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (231)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (234)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1379

```

```

Query Match      51.1%; Score 746; DB 3; Length 239;
Best Local Similarity 97.4%; Pred. No. 2,2e-63;
Matches 149; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      1 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIOPADDMQEFTEPKTKGR 60
Db      86 MSMPDAMPPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIOPADDMQEFTEPKTKGR 145
QY      61 RLSRSRISQSTSTSYSSAASYTDSDDVSPREKQNTNSGSSNFCVKNIKQAEFGREI 120
Db      146 RLSRSRISQSTSTSYSSAASYTDSDDVSPREKQNTNSGSSNFCVKNIKQAEFGREI 205
QY      121 EIAEODMSALISLRKRAQGEKPLAGAKIVGCTH 153
Db      206 EIAEODMSALISLRKRAQGEKPLGXKIXGLTH 238

```

```

RESULT 14
US-10-424-599-212758
; Sequence 212758, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

```

```

; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 212758
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(257)
; OTHER INFORMATION: unsure at all Xaa locations
; OTHER INFORMATION: Clone ID: PAT_MRT3847_34146C.1.pep
US-10-424-599-212758

```

```

Query Match      41.8%; Score 610.5; DB 4; Length 257;
Best Local Similarity 66.7%; Pred. No. 2.9e-50;
Matches 130; Conservative 17; Mismatches 21; Indels 27; Gaps 3;

```

```

QY      8 PLPGVGE-----ELKQAKEIEDAEKYSFMATVTKAPK--K 40
Db      63 PARGPSGPTAALSPAAGKVPQASAMKRSDDPHQHQRHRCGBALVSPDGTVEAPRTVK 122
QY      41 QIOPADDMQEFTEPKTKGRSLSRSISQSTSTSYSSAASYTDSDDVSPREKQNTNSK 100
Db      123 KIOPADQKQEFNRPKIGRSLSRSISQSTSTSYSSAASYTDSDDVSPREKQNTNSK 182
QY      101 GSSNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHITQATV 160
Db      183 GSSDFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHITQATV 242
QY      161 LIETLCALGAQCRRWS 175
Db      243 LMETLALGAQCRRWA 257

```

```

RESULT 15
US-10-369-493-13881
; Sequence 13881, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfang
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 13881
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-13881

```

```

Query Match      37.6%; Score 549; DB 4; Length 469;
Best Local Similarity 55.6%; Pred. No. 5.9e-44;
Matches 100; Conservative 38; Mismatches 40; Indels 2; Gaps 1;

```

```

QY      103 SNFCVKNIKQAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHITQATV 162
Db      11 NDYKVAADISLAMGRREITIAESEMPLMGLRKVASEQPLKAKILGCHIMTITQAVLI 70
QY      163 ETLCALGAQCRRWSACNIYSTQNEVVAALAEAGVAVFAMKGESEDDFWMCIDRCVNMNDG-- 220
Db      71 ETLVALGAQVRRWSCNIFSTQDPAASIAAGIPVAMKGETEEYEMCIEGTILDXGQP 130

```

QY 221 WQANMILDDGDLTHWYKYPNVFKKIRGIVESVTGVHRLYQLSKAGKLCVPANVND 280
DB 131 WQANMILDDGDLTELHKKYPOVLDRVHGVTEETTTGVHRLDMLAKGELKIPAINVND 190

Search completed: September 6, 2006, 19:57:42
Job time : 94.1304 secs

GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: September 6, 2006, 19:52:50 ; Search time 16.1304 Seconds
(without alignments)
1219.430 Million cell updates/sec

Title: US-10-683-610-1_COPY_1_280
Perfect score: 1461
Sequence: 1 MSMPAMPPLPGVGEELKQAK.....RLYQSKAGKLCVPMNVND 280

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 254368 seqs, 70249769 residues

Total number of hits satisfying chosen parameters: 254368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NMW_PUB.pep.*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NMW_PUB.pep.*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NMW_PUB.pep.*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NMW_PUB.pep.*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCR_NMW_PUB.pep.*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NMW_PUB.pep.*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NMW_PUB.pep.*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NMW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	509	34.8	439	US-10-449-902-37078	Sequence 37078, A
2	442	30.3	485	US-10-449-902-43217	Sequence 43217, A
3	100	6.8	787	US-10-449-902-45166	Sequence 45166, A
4	98	6.7	913	US-10-449-902-41150	Sequence 41150, A
5	97	6.6	291	US-10-953-349-5927	Sequence 5927, Ap
6	95	6.5	414	US-11-134-228A-28	Sequence 28, Appl
7	94	6.4	1206	US-10-953-349-16463	Sequence 16463, A
8	94	6.4	1210	US-10-953-349-16462	Sequence 16462, A
9	94	6.4	1129	US-10-953-349-16461	Sequence 16461, A
10	93.5	6.4	1129	US-10-449-902-43902	Sequence 43902, A
11	92	6.3	524	US-10-449-902-51179	Sequence 51179, A
12	92	6.3	602	US-10-449-902-54863	Sequence 54863, A
13	92	6.3	602	US-10-449-902-35242	Sequence 35242, A
14	91	6.2	685	US-10-374-780A-1583	Sequence 1583, Ap
15	90.5	6.2	255	US-11-056-355B-7413	Sequence 7413, Ap
16	90.5	6.2	602	US-11-056-355B-96044	Sequence 96044, A
17	90.5	6.2	619	US-11-056-355B-96043	Sequence 96043, A
18	90.5	6.2	636	US-11-056-355B-96042	Sequence 96042, A
19	89	6.1	319	US-10-953-349-32055	Sequence 32055, A
20	89	6.1	319	US-11-056-355B-66390	Sequence 66390, A
21	89	6.1	414	US-10-953-349-32054	Sequence 32054, A
22	89	6.1	414	US-11-056-355B-66389	Sequence 66389, A
23	89	6.1	441	US-11-330-403-17536	Sequence 17536, A
24	87.5	6.0	204	US-10-449-902-29164	Sequence 29164, A
25	87.5	6.0	204	US-10-449-902-50961	Sequence 50961, A

25	87.5	6.0	742	7	US-11-056-355B-78304	Sequence 78304, A
27	87	6.0	248	7	US-11-293-697-2900	Sequence 2900, Ap
28	87	6.0	386	7	US-11-056-355B-41563	Sequence 41563, A
29	86.5	5.9	553	7	US-11-293-697-2495	Sequence 2495, Ap
30	86	5.9	251	7	US-11-056-355B-5199	Sequence 5199, Ap
31	86	5.9	302	7	US-11-056-355B-5198	Sequence 5198, Ap
32	86	5.9	966	6	US-10-449-902-41240	Sequence 41240, A
33	86	5.9	1935	6	US-10-480-962-6	Sequence 6, Appl
34	85.5	5.9	1264	7	US-11-289-102-206	Sequence 206, Appl
35	84.5	5.8	326	6	US-10-449-902-51352	Sequence 51352, A
36	84.5	5.8	656	6	US-10-449-902-53496	Sequence 53496, A
37	84.5	5.8	943	6	US-10-449-902-52181	Sequence 52181, A
38	84	5.7	473	6	US-10-449-902-33535	Sequence 33535, A
39	84	5.7	581	6	US-10-449-902-31284	Sequence 31284, A
40	84	5.7	581	6	US-10-449-902-47568	Sequence 47568, A
41	84	5.7	1087	6	US-10-449-902-45269	Sequence 45269, A
42	84	5.7	1442	7	US-11-330-403-11957	Sequence 11957, A
43	84	5.7	2630	7	US-11-056-355B-45275	Sequence 45275, A
44	84	5.7	2677	7	US-11-056-355B-45274	Sequence 45274, A
45	84	5.7	2686	7	US-11-056-355B-45273	Sequence 45273, A

ALIGNMENTS

```

RESULT 1
US-10-449-902-37078
; Sequence 37078, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT DNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449, 902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37078
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Oryza sativa
;
US-10-449-902-37078
;
Query Match      34.8%; Score 509; DB 6; Length 439;
Best Local Similarity 53.3%; Pred. No. 7.6e-34;
Matches 98; Conservative 36; Mismatches 42; Indels 8; Gaps 2;

103 SNFCYKNIKQKQFGRREIEIAQDMISLQKRAQGEPLAGAKIVGCTHTTAOTAVLI 162
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2  SOYKVRDLSLEWGRKELELANEMPGIMETIRREYSAAQPLGARIAGLGHMTVOTAVLI 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
163 ETLTCAIGACRSPASCNISTONEVAALAEAGVAFAMWGESEDDFWWCIDRCVNDGW- 221
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
62 ETLTCAIGAEVRSSCNISTNDAAAALAKGIPFAWKGTEEEEDWDICGTIR--GPT 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
222 ----QANNILDDGDLTHWYKYPVNFKTRGVESVTVGHRLYQSKAGKLCVPM 276
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
120 TGGDTHPNNIILDDGDLTNLLINKHPEIAKIVGISEETTTGVKNLMKRVKAGTLTIPI 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      277 NVND 280
Db      180 NVND 183

RESULT 2
US-10-449-902-43217

```

; Sequence 43217, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43217
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-43217

Query Match 30.3%; Score 442; DB 6; Length 485;
Best Local Similarity 39.5%; Pred. No. 2.6e-28;
Matches 90; Conservative 41; Mismatches 53; Indels 44; Gaps 3;
QY 95 OOTNSGSSNFCVKNIKOAEFGREIEIAEODMSALISLRKRAQGEKPLAGAKIVGCTHI 154
DB 6 EKTSS--GREYKKDLSQADFGLEIEIAEVEHFGMLACAEFGSPQFPFGAISGLH 63
QY 155 TAQTAVLIETLCALGAQCRMSACNIVSTONVAAALAEAGVAVFAWKGESEDDFWMCIDR 214
DB 64 TIGTAVLIETLFTALGAEVWCSNIFSTODHAAALARDSAVFAWKGETLEEWCTER 123
QY 215 CVMND-GMQAMTLDGCGDLTHVYK----- 229
DB 124 CLDMGVGGPDLVDGSGATLLIHGVKAAEEFEKSGKVPDESDTDMAEKIVLTIND 183
QY 240 -----KYPNVFKIRGIYESVTGVHRLYQLSKAKLCPVPMNVND 280
DB 184 GLKSDSKTKRKMERLVGVSEETTTGVKRLYQWQERFALLFPAINVD 231

RESULT 3
US-10-449-902-45166
; Sequence 45166, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45166
; LENGTH: 787
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-45166

Query Match 6.8%; Score 100; DB 6; Length 787;
Best Local Similarity 22.9%; Pred. No. 4.1;
Matches 52; Conservative 31; Mismatches 70; Indels 74; Gaps 11;

QY 4 PPAIMPVGEBELKQAKIEDAEKYSFMATVTKAPKKQIQFADDMQEFKFPKTKGRSL 63
DB 421 PAACILSGIA--LSEAFDV-----LTRSVYQUS-----KLFDSPPAAG--DS 460
QY 64 SSISSGSTRDSYSAASYDSSDDEVSPEKQOTNSKGSNFCVKNIKOAEFGREIEIA 123
DB 461 SASSSASTVSTNSANETREPKETETAPKEKSKNR-----KEKEVA 504
QY 124 EODMSALISLRKRAQGEKPL---AGAKIVGCTHITTAQTAVLIETLCALG---AQCRMS 175
DB 505 E-----SVPAKPKKEXKLLVLPMEASVLG-----ILLIIVGGFFVYHCWA 546
QY 176 ACNIVSTONVAAALAEAGVAVF-----ANKGESEDDFWMCIDR 210
DB 547 AAEAVSAPSIIVLTSRSDGLHVFDDFREAYAVLISHTDQDVKASW 593

RESULT 4
US-10-449-902-41150
; Sequence 41150, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; PRIOR FILING DATE: 2002-12-11
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41150
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-41150

Query Match 6.7%; Score 98; DB 6; Length 913;
Best Local Similarity 21.2%; Pred. No. 7.3;
Matches 51; Conservative 35; Mismatches 74; Indels 80; Gaps 8;
QY 8 PLPGVGEELKQAKIEDAEKYSFMATVTKAPKK---QIQFA-----DMQOE 50
DB 329 PEGGLETVPRQREVDGAEGQLSSGAE-SVAPLKNPLSATFAPPESSASPETGDEORE 387
QY 51 FTKFPTKGRSLRSISGSTRDSYSAASYDSSDDE----- 88
DB 388 QEAGCGSSSSSSSSRS-SQSTDSRGNSAGSMWDOEDQVTAIFKPGGRWQKLKENG 446
QY 89 VSPREQOTNSGSSNFCVKNIKOAEFGREIEIAEODMSALISLRKRAQGEKPL 143
DB 447 IKSREERESEROGAAEASITWEAO--QQLATISEKNOLMNSGRLAASERKDEBEL 503
QY 144 AGAKIVGCTHITTAQTAVLIETLCALGAQCRMSACNIVSTONVAAALAEAGVAVFAWKGE 203
DB 504 ANLSLV-----ADDEAAKAAABAADSLMKSK 532

RESULT 5
US-10-953-349-5927
; Sequence 5927, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349


```
Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; PRIOR FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16461
; LENGTH: 1383
; TYPE: PRF
; ORGANISM: Glycine max
US-10-953-349-16461

Query Match
Best Local Similarity 21.4%; Score 94; DB 6; Length 1383;
Matches 63; Conservative 49; Mismatches 108; Indels 74; Gaps 16;

QY 16 LKANEIEDAEKYSFMATYTKAPKQIQ-PADMGEPTK--PPTKGRRS--LSRSISQS 70
DB 1107 VKWVAELDEPAEQNY---VKKHASEOALGVVREBAATFIFSNAGSGSYSNINLAIVENS 1163
QY 71 S-----TDSYSSAASYTDSDE---VSPREKQOTNSKSGSNFCVKNIKKAEFRREI 120
DB 1164 SWNDEKQLODMYISRSFAPSDAPAGAMTEKRAKVEFEMALSTADATFONDSEISLTDV 1223
QY 121 -EIAEODMSALI-SLRKRAOGEKPLAGAKIVGCTHTTAOTAVLIETLCALGAOCRSACN 178
DB 1224 SHYFSDPFTNVQNLARK--DGKKP--SAYIADTTTNAQVRLTSEIV-RIDATTKLLNPK 1278
QY 179 IYSTONEVAAALAEAGVAVFAWKGSEDEDFWMCIDCVANMDGQANMLDDGGDLTHWY 238
DB 1279 WYE-----GMLSTGYEGVREIE---KRLTIVGWSAT---SQQVNVWY 1316
QY 239 KK-----YPNVFKKI-----RGIVESYVGVHLYOL 265
DB 1317 EENATTFIODEOMLAKMLMSTNPSPKRLVOTFLEANGRGWETSEDNIEKRLQL 1370

RESULT 10
US-10-449-902-43902
; Sequence 43902, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43902
; LENGTH: 1129
; TYPE: PRF
; ORGANISM: Oryza sativa
US-10-449-902-43902

Query Match
Best Local Similarity 19.0%; Score 93.5; DB 6; Length 1129;
Matches 44; Conservative 33; Mismatches 75; Indels 79; Gaps 9;

QY 55 PRTKGRRS---LSRSISQSTDS-----SYSSAASYTDSDDVEVSPRE----- 93
DB 567 PSVTNRNEDLVNLTQARHSKSDENLTQERGMOSQHGTLTSLNADPDDHASFSAPVETDL 626
```

```
QY 94 ----KOOTNSKSSNFCVKNIKKAEFRREIEIAEODMSALISLRKAOGEKPLAGAKIV 149
DB 627 VLCTPRDCSSKSSSYCRKVBDE---RSVHLVPRKVDL-LLKHPQDSVQP----- 675
QY 150 GCCHITPAQTAVLIETLCALGAOCRSACNIYSTONEVAAALAEAGVAVFA-WKGESEDDF 208
DB 676 -----NCSMSINVGKTSHTLSHVSAGGFSATGOMKRSF--- 712
QY 209 WMCIDRCVNMMDGQANMLDDGGDLTHWYKKYPNVFKKIRGIVESYTVG 259
DB 713 -----LAAQNSDLN--YKLLVERLFRVGVGQREAVSAI 744

RESULT 11
US-10-449-902-51179
; Sequence 51179, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
; TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
; FILE REFERENCE: MOA-A0205Y1-US
; CURRENT APPLICATION NUMBER: US/10/449,902
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: JP 2002-203269
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: JP 2002-383870
; NUMBER OF SEQ ID NOS: 56791
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51179
; LENGTH: 445
; TYPE: PRF
; ORGANISM: Oryza sativa
US-10-449-902-51179

Query Match
Best Local Similarity 25.6%; Score 92; DB 6; Length 445;
Matches 67; Conservative 30; Mismatches 109; Indels 56; Gaps 13;

QY 14 EELKQAK-----EIEDAEKYSFMATYTKAPKQIQRAD-----DMOEF 51
DB 83 DELKAKKEQLSSESRRRHTQEAERAKQEDPAT-SKEDLQROIAEFSAAEESRLQEL 141
QY 52 TFPPTKGRRSLSRSISQSTDSYSSAASYTDSDDVEVSPREKQOTNSKSSNFCVKNIK 111
DB 142 RYVSQERDPAWSELEAVYKQOSVBSAA--LSALSIEIQ-RLKQOUGATTESD--AARAK 196
QY 112 QAEFRREIEIAEODMS--ALISLRKRAOGEKPLAGAKIVGCTHTTAOT-----AVL 161
DB 197 QCEFAESELEGGKQEMELRLATIEGLKVNVGESDPAVAE--ANVVAETKQOLEMAOAT 253
QY 162 IETLCALGAOCRSACNIYSTONEVAAALAEAGVAVFAWKGSEDEDFWMCIDRCVNMMDG 221
DB 254 IDSLAEBA--RLQER-LRSKDAELGQSWARLALT-----EED---LKKAHKDDV 258
QY 222 QANMLDDGGDLTHWYKKYYPN 243
DB 299 DGSFSPDHGAVERKVVITPN 320

RESULT 12
US-10-449-902-54863
; Sequence 54863, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
; APPLICANT: National Institute of Agrobiological Sciences.
; APPLICANT: Bio-oriented Technology Research Advancement Institution.
; APPLICANT: The Institute of Physical and Chemical Research.
; APPLICANT: Foundation for Advancement of International Science.
```

; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 54863
 ; LENGTH: 524
 ; TYPE: PRF
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-54863

Query Match 6.3%; Score 92; DB 6; Length 524;
 Best Local Similarity 25.6%; Pred. No. 11;
 Matches 67; Conservative 30; Mismatches 109; Indels 56; Gaps 13;

QY 14 BELKQAK-----EIEDAEKYSFMAVTYTKAPKQIQPAD-----DMQEF 51
 DB 83 DELKAKAEQLSSESRRHTQOEAEBAKQEQOAT-SKLEDIQRQLAEFSABESRLQEL 141
 QY 52 TFPPTKGRSLSRSISQSTDSYSSAASYTDSDEVPREKQOTNSKSSNFCVKNIK 111
 DB 142 RYVSLEPDAWSELEAVKQOSVDSAA--LSSALSEIO-RLKQOQAGATTESD--AARAK 196
 QY 112 QAEFGREIEIAEODMS--ALISLRKRAQGEKPLAGAKIVGCTHTTAOT-----AVL 161
 DB 197 QCEFAESELEGLKQEMELRLATIEGLKVNAGSDKVAE--ANAVAAETKQOLEMAQAT 253
 QY 162 IETLCALGAQCWSACNIVSTONENVAALAEAGVAFPAWKGSEDDFWMCIDRCVMMGW 221
 DB 254 IDSLAEGA--RLQEC-LRSKDAELGQSWARLATL-----EED-----LKKAHNKDV 298
 QY 222 QANMILDDGGDLTHWYKYPN 243
 DB 299 DGSFGSPDHGEAVEKVVITPN 320

RESULT 13
 US-10-449-902-35242
 ; Sequence 35242, Application US/104499902
 ; Publication No. US20060123505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: National Institute of Agricultural Sciences.
 ; APPLICANT: Bio-oriented Technology Research Advancement Institution.
 ; APPLICANT: The Institute of Physical and Chemical Research.
 ; APPLICANT: Foundation for Advancement of International Science.
 ; TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF.
 ; FILE REFERENCE: MOA-A0205Y1-US
 ; CURRENT APPLICATION NUMBER: US/10/449,902
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: JP 2002-203269
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: JP 2002-383870
 ; PRIOR FILING DATE: 2002-12-11
 ; NUMBER OF SEQ ID NOS: 56791
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 35242
 ; LENGTH: 602
 ; TYPE: PRF
 ; ORGANISM: Oryza sativa
 ; US-10-449-902-35242

Query Match 6.3%; Score 92; DB 6; Length 602;
 Best Local Similarity 25.6%; Pred. No. 13;
 Matches 67; Conservative 30; Mismatches 109; Indels 56; Gaps 13;

QY 52 TFPPTKGRSLSRSISQSTDSYSSAASYTDSDEVPREKQOTNSKSSNFCVKNIK 111
 DB 141 RYVSLEPDAWSELEAVKQOSVDSAA--LSSALSEIO-RLKQOQAGATTESD--AARAK 195
 QY 112 QAEFGREIEIAEODMS--ALISLRKRAQGEKPLAGAKIVGCTHTTAOT-----AVL 161
 DB 196 QCEFAESELEGLKQEMELRLATIEGLKVNAGSDKVAE--ANAVAAETKQOLEMAQAT 252
 QY 162 IETLCALGAQCWSACNIVSTONENVAALAEAGVAFPAWKGSEDDFWMCIDRCVMMGW 221
 DB 253 IDSLAEGA--RLQEC-LRSKDAELGQSWARLATL-----EED-----LKKAHNKDV 297
 QY 222 QANMILDDGGDLTHWYKYPN 243
 DB 298 DGSFGSPDHGEAVEKVVITPN 319

RESULT 14
 US-10-374-780A-1583
 ; Sequence 1583, Application US/10374780A
 ; Publication No. US20060162006A9
 ; GENERAL INFORMATION:
 ; APPLICANT: Sherman, Bradley K
 ; APPLICANT: Riechmann, Jose Luis
 ; APPLICANT: Jiang, Cai-Zhong
 ; APPLICANT: Heard, Jacqueline E
 ; APPLICANT: Haake, Volker
 ; APPLICANT: Creeliman, Robert A
 ; APPLICANT: Ratcliffe, Oliver
 ; APPLICANT: Adam, Luc J
 ; APPLICANT: Reuber, T. Lynne
 ; APPLICANT: Reddie, James
 ; APPLICANT: Brown, Pierre E
 ; APPLICANT: Pilgrim, Marsha L
 ; APPLICANT: Dubell III, Arnold T
 ; APPLICANT: Pineda, Omaira
 ; APPLICANT: Yu, Guo-Liang
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
 ; FILE REFERENCE: MBI-0047 CIP
 ; CURRENT APPLICATION NUMBER: US/10/374,780A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: 09/837,944
 ; PRIOR FILING DATE: 2001-04-18
 ; PRIOR APPLICATION NUMBER: 60/310,847
 ; PRIOR FILING DATE: 2001-08-09
 ; PRIOR APPLICATION NUMBER: 09/934,455
 ; PRIOR FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/336,049
 ; PRIOR FILING DATE: 2001-11-19
 ; PRIOR APPLICATION NUMBER: 60/338,692
 ; PRIOR FILING DATE: 2001-12-11
 ; PRIOR APPLICATION NUMBER: 10/171,468
 ; PRIOR FILING DATE: 2002-06-14
 ; PRIOR APPLICATION NUMBER: 10/225,066
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/225,067
 ; PRIOR FILING DATE: 2002-08-09
 ; PRIOR APPLICATION NUMBER: 10/225,068
 ; PRIOR FILING DATE: 2002-08-09
 ; NUMBER OF SEQ ID NOS: 2906
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 1583
 ; LENGTH: 685
 ; TYPE: PRF
 ; ORGANISM: Oryza sativa
 ; OTHER INFORMATION: Orthologous to G1363
 ; US-10-374-780A-1583

Query Match 6.2%; Score 91; DB 6; Length 685;
 Best Local Similarity 23.5%; Pred. No. 19;
 Matches 44; Conservative 26; Mismatches 69; Indels 48; Gaps 6;

```
QY      19 AKIEDAEKXSFNATV--TKAPKKQIQFADDMQEFTEPKTKT-----G 59
      100 AQASDAIAIAAAATTSKSVPRGRKFSVLAGNRKRKTPPSALDASPPPPRRRLVTLG 159
QY      60 RRLSLRSISGSSSTDSYSSASTDSSPDEVSPREKQOTNSKSSNF----- 105
      160 EKARARAAQDGGSGNSSASPAVASTDVVAPRSREVTGPGPASDLVGRGPPAAVLTWE 219
QY      106 -----CVNNIKQAEFGREI--EIAEQDMSALISLRKRAQG-EKPLAGAKIVGCTHIT 155
      220 ELQVEMGCI-----LEAGARGISREIVEARAAASASNERADKLARDLAETVYTGHLQLT 274
QY      156 AQTAVLI 162
      275 GECGVMI 281
Db
```

```
RESULT 15
US-11-056-355B-7413
; Sequence 7413, Application US/11056355B
; Publication No. US20060150283A1
; GENERAL INFORMATION:
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nikolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; FILE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 7413
; LENGTH: 255
; TYPE: PTC
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(255)
; OTHER INFORMATION: Ceres Seq. ID no. 12353934
US-11-056-355B-7413
```

```
Query Match      6.24; Score 90.5; DB 7; Length 255;
Best Local Similarity 26.04; Pred. No. 5.7;
Matches 40; Conservative 27; Mismatches 68; Indels 19; Gaps 5;
```

```
QY      64 SRIS-----QSTDSYSSASASTDSSPDEVSPREKQOTNSKSSNFCVKNIKQAEFG 116
      60 SRIVSTSGGGGDDLTDLLEAKRSKTKNSNNKGSILRTEVETDSRSAGKAVSKNIPAAEP 119
QY      117 RRE---IEIAEQDMSALISLRKRAQGEKPLAGAKIV-----GCTHITPQAVLIETL 168
      120 KQDIYHVRARQATDSDHSLAERARRKREISERMKVLODVLPGCNKVIKASVLDLITINYI 179
Db      169 -GAQCRMSACNIYSTONEVAALAEAGVAVPAWK 201
      180 QSLQCG---VEFLSMKLEAVNAQANQGVAVPAK 210
QY
```

Search completed: September 6, 2006, 19:58:40
Job time : 17.1304 secs